SEQUENCE LISTING

<110> Jensen, Michael

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<300>
<301> Collart,F.R. and Huberman,E.
<302> Cloning and sequence analysis of the human and
<303> J. Biol. Chem. (1988)
<304> 263
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Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr
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gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt         152
Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe
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ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg         200
Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu
                40                  45                  50

act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg gtt tcc         248
Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu Val Ser
            55                  60                  65

tct ccc atg gac aca gtc aca gag gct ggg atg gcc ata gca atg gcg         296
Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile Ala Met Ala
            70                  75                  80

ctt aca ggc ggt att ggc ttc atc cac cac aac tgt aca cct gaa ttc         344
Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro Glu Phe
    85                  90                  95
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cag gcc aat gaa gtt cgg aaa gtg aag aaa tat gaa cag gga ttc atc    392
Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln Gly Phe Ile
100             105             110             115

aca gac cct gtg gtc ctc agc ccc aag gat cgc gtg cgg gat gtt ttt    440
Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg Asp Val Phe
            120             125             130

gag gcc aag gcc cgg cat ggt ttc tgc ggt atc cca atc aca gac aca    488
Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile Thr Asp Thr
        135             140             145

ggc cgg atg ggg agc cgc ttg gtg ggc atc atc tcc tcc agg gac att    536
Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser Arg Asp Ile
        150             155             160

gat ttt ctc aaa gag gag gaa cat gac tgt ttc ttg gaa gag ata atg    584
Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu Glu Ile Met
    165             170             175

aca aag agg gaa gac ttg gtg gta gcc ccc cgc agc atc aca ctg aag    632
Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile Thr Leu Lys
180             185             190             195

gag gca aat gaa att ctg cag cgc agc aag aag gga aag ttg ccc att    680
Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys Leu Pro Ile
            200             205             210

gta aat gaa gat gat gag ctt gtg gcc atc att gcc cgg aca gac ctg    728
Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg Thr Asp Leu
        215             220             225

aag aag aat cgg gac tac cca cta gcc tcc aaa gat gcc aag aaa cag    776
Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala Lys Lys Gln
        230             235             240

ctg ctg tgt ggg gca gcc att ggc act cat gag gat gac aag tat agg    824
Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp Lys Tyr Arg
245             250             255

ctg gac ttg ctc gcc cag gct ggt gtg gat gta gtg gtt ttg gac tct    872
Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu Asp Ser
260             265             270             275

tcc cag gga aat tcc atc ttc cag atc aat atg atc aag tac atc aaa    920
Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys Tyr Ile Lys
            280             285             290

gac aaa tac cct aat ctc caa gtc att gga ggc aat gtg gtc act gct    968
Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val Thr Ala
            295             300             305

gcc cag gcc aag aac ctc att gat gca ggt gtg gat gcc ctg cgg gtg    1016
Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu Arg Val
        310             315             320

ggc atg gga agt ggc tcc atc tgc att acg cag gaa gtg ctg gcc tgt    1064
Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala Cys
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ggg cgg ccc caa gca aca gca gtg tac aag gtg tca gag tat gca cgg    1112
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Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu Tyr Ala Arg
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cgc ttt ggt gtt ccg gtc att gct gat gga gga atc caa aat gtg ggt      1160
Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn Val Gly
                360             365             370

cat att gcg aaa gcc ttg gcc ctt ggg gcc tcc aca gtc atg atg ggc      1208
His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met .Met Gly
            375             380             385

tct ctc ctg gct gcc acc act gag gcc cct ggt gaa tac ttc ttt tcc      1256
Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr Phe Phe Ser
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gat ggg atc cgg cta aag aaa tat cgc ggt atg ggt tct ctc gat gcc      1304
Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser Leu Asp Ala
    405             410             415

atg gac aag cac ctc agc agc cag aac aga tat ttc agt gaa gct gac      1352
Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu Ala Asp
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aaa atc aaa gtg gcc cag gga gtg tct ggt gct gtg cag gac aaa ggg      1400
Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp Lys Gly
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Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile Gln His Ser
            455             460             465

tgc cag gac att ggt gcc aag agc ttg acc caa gtc cga gcc atg atg      1496
Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala Met Met
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tac tct ggg gag ctt aag ttt gag aag aga acg tcc tca gcc cag gtg      1544
Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala Gln Val
    485             490             495

gaa ggt ggc gtc cat agc ctc cat tcg tat gag aag cgg ctt ttc          1589
Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu Phe
500             505             510

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<212> PRT
<213> Homo sapien

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Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
        35              40              45
Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
    50              55              60
Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
65              70              75              80
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Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
                85                  90                      95
Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
            100             105             110
Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
        115             120             125
Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
    130             135             140
Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
145             150             155             160
Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu
                165             170             175
Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile
            180             185             190
Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
        195             200             205
Leu Pro Ile Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg
    210             215             220
Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
225             230             235             240
Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
                245             250             255
Lys Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val
            260             265             270
Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
        275             280             285
Tyr Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val
    290             295             300
Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
305             310             315             320
Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val
                325             330             335
Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu
            340             345             350
Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
        355             360             365
Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
    370             375             380
Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
385             390             395             400
Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
            405             410             415
Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser
        420             425             430
Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
        435             440             445
Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
    450             455             460
Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg
465             470             475             480
Ala Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser
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Leu Phe
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<210> 3
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                                                    Met Ala Asp
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tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga ctc aca         104
Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr
     5                  10                  15

gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt         152
Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe
 20                  25                  30                  35

ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg         200
Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu
                 40                  45                  50

act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg gtt tcc         248
Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu Val Ser
             55                  60                  65

tct ccc atg gac aca gtc aca gag gct ggg atg gcc ata gca atg gcg         296
Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile Ala Met Ala
         70                  75                  80

ctt aca ggc ggt att ggc ttc atc cac cac aac tgt aca cct gaa ttc         344
Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro Glu Phe
         85                  90                  95

cag gcc aat gaa gtt cgg aaa gtg aag aaa tat gaa cag gga ttc atc         392
Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln Gly Phe Ile
100                 105                 110                 115

aca gac cct gtg gtc ctc agc ccc aag gat cgc gtg cgg gat gtt ttt         440
Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg Asp Val Phe
                 120                 125                 130

gag gcc aag gcc cgg cat ggt ttc tgc ggt atc cca atc aca gac aca         488
Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile Thr Asp Thr
         135                 140                 145
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ggc cgg atg ggg agc cgc ttg gtg ggc atc atc tcc tcc agg gac att    536
Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser Arg Asp Ile
        150             155             160

gat ttt ctc aaa gag gag gaa cat gac tgt ttc ttg gaa gag ata atg    584
Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu Glu Ile Met
    165             170             175

aca aag agg gaa gac ttg gtg gta gcc ccc cgc agc atc aca ctg aag    632
Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile Thr Leu Lys
180             185             190             195

gag gca aat gaa att ctg cag cgc agc aag aag gga aag ttg ccc att    680
Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys Leu Pro Ile
                200             205             210

gta aat gaa gat gat gag ctt gtg gcc atc att gcc cgg aca gac ctg    728
Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg Thr Asp Leu
            215             220             225

aag aag aat cgg gac tac cca cta gcc tcc aaa gat gcc aag aaa cag    776
Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala Lys Lys Gln
        230             235             240

ctg ctg tgt ggg gca gcc att ggc act cat gag gat gac aag tat agg    824
Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp Lys Tyr Arg
    245             250             255

ctg gac ttg ctc gcc cag gct ggt gtg gat gta gtg gtt ttg gac tct    872
Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu Asp Ser
260             265             270             275

tcc cag gga aat tcc atc ttc cag atc aat atg atc aag tac atc aaa    920
Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys Tyr Ile Lys
                280             285             290

gac aaa tac cct aat ctc caa gtc att gga ggc aat gtg gtc act gct    968
Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val Thr Ala
            295             300             305

gcc cag gcc aag aac ctc att gat gca ggt gtg gat gcc ctg cgg gtg    1016
Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu Arg Val
        310             315             320

ggc atg gga agt ggc tcc atc tgc att atc cag gaa gtg ctg gcc tgt    1064
Gly Met Gly Ser Gly Ser Ile Cys Ile Ile Gln Glu Val Leu Ala Cys
    325             330             335

ggg cgg ccc caa gca aca gca gtg tac aag gtg tat gag tat gca cgg    1112
Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Tyr Glu Tyr Ala Arg
340             345             350             355

cgc ttt ggt gtt ccg gtc att gct gat gga gga atc caa aat gtg ggt    1160
Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn Val Gly
                360             365             370

cat att gcg aaa gcc ttg gcc ctt ggg gcc tcc aca gtc atg atg ggc    1208
His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met Met Gly
            375             380             385

tct ctc ctg gct gcc acc act gag gcc cct ggt gaa tac ttc ttt tcc    1256
Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr Phe Phe Ser
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                390                    395                    400
gat ggg atc cgg cta aag aaa tat cgc ggt atg ggt tct ctc gat gcc      1304
Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser Leu Asp Ala
    405                    410                    415

atg gac aag cac ctc agc agc cag aac aga tat ttc agt gaa gct gac      1352
Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu Ala Asp
420                    425                    430                435

aaa atc aaa gtg gcc cag gga gtg tct ggt gct gtg cag gac aaa ggg      1400
Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp Lys Gly
                   440                    445                    450

tca atc cac aaa ttt gtc cct tac ctg att gct ggc atc caa cac tca      1448
Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile Gln His Ser
                   455                    460                    465

tgc cag gac att ggt gcc aag agc ttg acc caa gtc cga gcc atg atg      1496
Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala Met Met
        470                    475                    480

tac tct ggg gag ctt aag ttt gag aag aga acg tcc tca gcc cag gtg      1544
Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala Gln Val
    485                    490                    495

gaa ggt ggc gtc cat agc ctc cat tcg tat gag aag cgg ctt ttc         1589
Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu Phe
500                    505                    510

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<211> 514
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Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
               35                   40                   45
Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
    50                   55                   60
Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
65                   70                   75                   80
Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
               85                   90                   95
Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
               100                  105                  110
Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
               115                  120                  125
Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
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Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
145                  150                  155                  160
Arg Asp Ile Asp Phe Leu Lys Glu Glu His Asp Cys Phe Leu Glu
               165                  170                  175
Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile
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Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
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Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
225                     230                     235                 240
Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
            245                     250                     255
Lys Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val
        260                     265                     270
Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
        275                     280                     285
Tyr Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val
    290                     295                     300
Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
305                     310                     315                 320
Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Ile Gln Glu Val
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Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Tyr Glu
        340                     345                     350
Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
        355                     360                     365
Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
    370                     375                     380
Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
385                     390                     395                 400
Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
            405                     410                     415
Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser
        420                     425                     430
Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
        435                     440                     445
Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
    450                     455                     460
Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg
465                     470                     475                 480
Ala Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser
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Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg
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Leu Phe
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Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr
        5                   10                  15

gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt          152
Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe
20                  25                  30                  35

ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg          200
Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu
                40                  45                  50

act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg gtt tcc          248
Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu Val Ser
                55                  60                  65

tct ccc atg gac aca gtc aca gag gct ggg atg gcc ata gca atg gcg          296
Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile Ala Met Ala
                70                  75                  80

ctt aca ggc ggt att ggc ttc atc cac cac aac tgt aca cct gaa ttc          344
Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro Glu Phe
        85                  90                  95

cag gcc aat gaa gtt cgg aaa gtg aag aaa tat gaa cag gga ttc atc          392
Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln Gly Phe Ile
100                 105                 110                 115

aca gac cct gtg gtc ctc agc ccc aag gat cgc gtg cgg gat gtt ttt          440
Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg Asp Val Phe
                120                 125                 130

gag gcc aag gcc cgg cat ggt ttc tgc ggt atc cca atc aca gac aca          488
Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile Thr Asp Thr
            135                 140                 145

ggc cgg atg ggg agc cgc ttg gtg ggc atc atc tcc tcc agg gac att          536
Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser Arg Asp Ile
            150                 155                 160

gat ttt ctc aaa gag gag gaa cat gac tgt ttc ttg gaa gag ata atg          584
Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu Glu Ile Met
            165                 170                 175

aca aag agg gaa gac ttg gtg gta gcc ccc cgc agc atc aca ctg aag          632
Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile Thr Leu Lys
180                 185                 190                 195

gag gca aat gaa att ctg cag cgc agc aag aag gga aag ttg ccc att          680
Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys Leu Pro Ile
                200                 205                 210

gta aat gaa gat gat gag ctt gtg gcc atc att gcc cgg aca gac ctg          728
Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg Thr Asp Leu
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                215                      220                      225

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Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala Lys Lys Gln
        230                      235                      240

ctg ctg tgt ggg gca gcc att ggc act cat gag gat gac aag tat agg      824
Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp Lys Tyr Arg
        245                      250                      255

ctg gac ttg ctc gcc cag gct ggt gtg gat gta gtg gtt ttg gac tct      872
Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu Asp Ser
260                      265                      270                      275

tcc cgg gga aat tcc atc ttc cag atc aat atg atc aag tac atc aaa      920
Ser Arg Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys Tyr Ile Lys
                280                      285                      290

gac aaa tac cct aat ctc caa gtc att gga ggc aat gtg gtc act gct      968
Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val Thr Ala
                295                      300                      305

gcc cag gcc aag aac ctc att gat gca ggt gtg gat gcc ctg cgg gtg     1016
Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu Arg Val
        310                      315                      320

ggc atg gga agt ggc tcc atc tgc att acg cag gaa gtg ctg gcc tgt     1064
Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala Cys
        325                      330                      335

ggg cgg ccc caa gca aca gca gtg tac aag gtg tca gag tat gca cgg     1112
Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu Tyr Ala Arg
340                      345                      350                      355

cgc ttt ggt gtt ccg gtc att gct gat gga gga atc caa aat gtg ggt     1160
Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn Val Gly
                360                      365                      370

cat att gcg aaa gcc ttg gcc ctt ggg gcc tcc aca gtc atg atg ggc     1208
His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met Met Gly
                375                      380                      385

tct ctc ctg gct gcc acc act gag gcc cct ggt gaa tac ttc ttt tcc     1256
Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr Phe Phe Ser
        390                      395                      400

gat ggg atc cgg cta aag aaa tat cgc ggt atg ggt tct ctc gat gcc     1304
Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser Leu Asp Ala
        405                      410                      415

atg gac aag cac ctc agc agc cag aac aga tat ttc agt gaa gct gac     1352
Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu Ala Asp
420                      425                      430                      435

aaa atc aaa gtg gcc cag gga gtg tct ggt gct gtg cag gac aaa ggg     1400
Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp Lys Gly
                440                      445                      450

tca atc cac aaa ttt gtc cct tac ctg att gct ggc atc caa cac tca     1448
Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile Gln His Ser
                455                      460                      465
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tgc cag gac att ggt gcc aag agc ttg acc caa gtc cga gcc atg atg    1496
Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala Met Met
        470                 475                 480

tac tct ggg gag ctt aag ttt gag aag aga acg tcc tca gcc cag gtg    1544
Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala Gln Val
        485                 490                 495

gaa ggt ggc gtc cat agc ctc cat tcg tat gag aag cgg ctt ttc        1589
Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu Phe
500                 505                 510

tgaaaaggga tccagcacac ctcctcggtt tttttttcaa taaaagttta gaaagacccg   1649
aattc                                                              1654
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<210> 6
<211> 514
<212> PRT
<213> Homo sapien

<400> 6

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Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
1                 5                  10                  15
Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
            20                  25                  30
Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
            35                  40                  45
Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
        50                  55                  60
Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
65                  70                  75                  80
Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
                85                  90                  95
Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
                100                 105                 110
Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
            115                 120                 125
Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
        130                 135                 140
Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
145                 150                 155                 160
Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu
                165                 170                 175
Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile
                180                 185                 190
Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
            195                 200                 205
Leu Pro Ile Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg
        210                 215                 220
Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
225                 230                 235                 240
Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
                245                 250                 255
Lys Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val
            260                 265                 270
Leu Asp Ser Ser Arg Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
            275                 280                 285
Tyr Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val
        290                 295                 300
Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
305                 310                 315                 320
Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val
```

```
                  325                     330                     335
Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu
              340                     345                     350
Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
          355                     360                     365
Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
      370                     375                     380
Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
385                     390                     395                 400
Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
              405                     410                     415
Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser
          420                     425                     430
Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
          435                     440                     445
Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
      450                     455                     460
Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg
465                     470                     475                 480
Ala Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser
              485                     490                     495
Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg
          500                     505                     510
Leu Phe
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<210> 7
<211> 1654
<212> DNA
<213> Homo sapien

<220>
<221> mutation
<222> 1431
<223> G to A mutation

<221> CDS
<222> (48)...(1589)
<223> Ala462Thr Human IMPDH II mutant

<300>
<301> Farazi et al.
<303> J. Biol. Chem. (1997)
<304> 272
<305> 2
<306> 961-965

<400> 7
gaattcgggc ggtcctcgga gacacgcggc ggtgtcctgt gttggcc atg gcc gac          56
                                                    Met Ala Asp
                                                     1

tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga ctc aca         104
Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr
     5                  10                  15

gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt         152
Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe
 20                  25                  30                      35

ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg         200
Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu
```

```
                    40                        45                        50
act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg gtt tcc        248
Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu Val Ser
            55                        60                    65

tct ccc atg gac aca gtc aca gag gct ggg atg gcc ata gca atg gcg        296
Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile Ala Met Ala
            70                    75                    80

ctt aca ggc ggt att ggc ttc atc cac cac aac tgt aca cct gaa ttc        344
Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro Glu Phe
        85                    90                    95

cag gcc aat gaa gtt cgg aaa gtg aag aaa tat gaa cag gga ttc atc        392
Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln Gly Phe Ile
100                 105                 110                 115

aca gac cct gtg gtc ctc agc ccc aag gat cgc gtg cgg gat gtt ttt        440
Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg Asp Val Phe
                120                 125                 130

gag gcc aag gcc cgg cat ggt ttc tgc ggt atc cca atc aca gac aca        488
Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile Thr Asp Thr
            135                 140                 145

ggc cgg atg ggg agc cgc ttg gtg ggc atc atc tcc tcc agg gac att        536
Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser Arg Asp Ile
            150                 155                 160

gat ttt ctc aaa gag gag gaa cat gac tgt ttc ttg gaa gag ata atg        584
Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu Glu Ile Met
            165                 170                 175

aca aag agg gaa gac ttg gtg gta gcc ccc cgc agc atc aca ctg aag        632
Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile Thr Leu Lys
180                 185                 190                 195

gag gca aat gaa att ctg cag cgc agc aag aag gga aag ttg ccc att        680
Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys Leu Pro Ile
                200                 205                 210

gta aat gaa gat gat gag ctt gtg gcc atc att gcc cgg aca gac ctg        728
Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg Thr Asp Leu
                215                 220                 225

aag aag aat cgg gac tac cca cta gcc tcc aaa gat gcc aag aaa cag        776
Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala Lys Lys Gln
            230                 235                 240

ctg ctg tgt ggg gca gcc att ggc act cat gag gat gac aag tat agg        824
Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp Lys Tyr Arg
            245                 250                 255

ctg gac ttg ctc gcc cag gct ggt gtg gat gta gtg gtt ttg gac tct        872
Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu Asp Ser
260                 265                 270                 275

tcc cag gga aat tcc atc ttc cag atc aat atg atc aag tac atc aaa        920
Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys Tyr Ile Lys
                280                 285                 290
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gac aaa tac cct aat ctc caa gtc att gga ggc aat gtg gtc act gct       968
Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val Thr Ala
            295                 300                 305

gcc cag gcc aag aac ctc att gat gca ggt gtg gat gcc ctg cgg gtg      1016
Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu Arg Val
            310                 315                 320

ggc atg gga agt ggc tcc atc tgc att acg cag gaa gtg ctg gcc tgt      1064
Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala Cys
            325                 330                 335

ggg cgg ccc caa gca aca gca gtg tac aag gtg tca gag tat gca cgg      1112
Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu Tyr Ala Arg
340                 345                 350                 355

cgc ttt ggt gtt ccg gtc att gct gat gga gga atc caa aat gtg ggt      1160
Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn Val Gly
                360                 365                 370

cat att gcg aaa gcc ttg gcc ctt ggg gcc tcc aca gtc atg atg ggc      1208
His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met Met Gly
            375                 380                 385

tct ctc ctg gct gcc acc act gag gcc cct ggt gaa tac ttc ttt tcc      1256
Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr Phe Phe Ser
            390                 395                 400

gat ggg atc cgg cta aag aaa tat cgc ggt atg ggt tct ctc gat gcc      1304
Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser Leu Asp Ala
            405                 410                 415

atg gac aag cac ctc agc agc cag aac aga tat ttc agt gaa gct gac      1352
Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu Ala Asp
420                 425                 430                 435

aaa atc aaa gtg gcc cag gga gtg tct ggt gct gtg cag gac aaa ggg      1400
Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp Lys Gly
                440                 445                 450

tca atc cac aaa ttt gtc cct tac ctg att act ggc atc caa cac tca      1448
Ser Ile His Lys Phe Val Pro Tyr Leu Ile Thr Gly Ile Gln His Ser
            455                 460                 465

tgc cag gac att ggt gcc aag agc ttg acc caa gtc cga gcc atg atg      1496
Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala Met Met
            470                 475                 480

tac tct ggg gag ctt aag ttt gag aag aga acg tcc tca gcc cag gtg      1544
Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala Gln Val
            485                 490                 495

gaa ggt ggc gtc cat agc ctc cat tcg tat gag aag cgg ctt ttc          1589
Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu Phe
500                 505                 510

tgaaaaggga tccagcacac ctcctcggtt tttttttcaa taaaagttta gaaagacccg     1649
aattc                                                                 1654
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<210> 8
<211> 514
<212> PRT
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<213> Homo sapien

<400> 8

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Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
1               5                   10              15
Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
            20                  25              30
Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
        35                  40                  45
Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
    50                  55                  60
Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
65                  70                  75                  80
Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
            85                  90                  95
Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
            100                 105                 110
Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
        115                 120                 125
Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
    130                 135                 140
Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
145                 150                 155                 160
Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu
                165                 170                 175
Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile
            180                 185                 190
Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
        195                 200                 205
Leu Pro Ile Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg
    210                 215                 220
Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
225                 230                 235                 240
Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
            245                 250                 255
Lys Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val
        260                 265                 270
Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
    275                 280                 285
Tyr Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val
    290                 295                 300
Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
305                 310                 315                 320
Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val
            325                 330                 335
Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu
            340                 345                 350
Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
        355                 360                 365
Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
    370                 375                 380
Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
385                 390                 395                 400
Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
                405                 410                 415
Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser
            420                 425                 430
Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
            435                 440                 445
Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Thr Gly Ile
    450                 455                 460
Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg
```

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465                     470                     475                     480
Ala Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser
                    485                     490                     495
Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg
                500                     505                     510
Leu Phe
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<210> 9
<211> 1654
<212> DNA
<213> Homo sapien

<220>
<221> mutation
<222> 877
<223> A to G mutation

<221> mutation
<222> 1431
<223> G to A mutation

<221> CDS
<222> (48)...(1589)
<223> Gln277Arg/Ala462Thr Human IMPDH II mutant

<300>
<301> Farazi et al.
<302> Isolation and Characterization of Mycophenolic
<303> J. Biol. Chem. (1997)
<304> 272
<305> 2
<306> 961-965

<400> 9
gaattcgggc ggtcctcgga gacacgcggc ggtgtcctgt gttggcc atg gcc gac      56
                                                     Met Ala Asp
                                                      1


tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga ctc aca     104
Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr
    5                   10                  15


gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt     152
Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe
20                  25                  30                      35


ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg     200
Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu
                40                  45                  50


act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg gtt tcc     248
Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu Val Ser
            55                  60                  65


tct ccc atg gac aca gtc aca gag gct ggg atg gcc ata gca atg gcg     296
Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile Ala Met Ala
            70                  75                  80


ctt aca ggc ggt att ggc ttc atc cac cac aac tgt aca cct gaa ttc     344
Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro Glu Phe
        85                  90                  95
```

-16 of 61-

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cag gcc aat gaa gtt cgg aaa gtg aag aaa tat gaa cag gga ttc atc    392
Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln Gly Phe Ile
100             105             110             115

aca gac cct gtg gtc ctc agc ccc aag gat cgc gtg cgg gat gtt ttt    440
Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg Asp Val Phe
            120             125             130

gag gcc aag gcc cgg cat ggt ttc tgc ggt atc cca atc aca gac aca    488
Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile Thr Asp Thr
        135             140             145

ggc cgg atg ggg agc cgc ttg gtg ggc atc atc tcc tcc agg gac att    536
Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser Arg Asp Ile
        150             155             160

gat ttt ctc aaa gag gag gaa cat gac tgt ttc ttg gaa gag ata atg    584
Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu Glu Ile Met
        165             170             175

aca aag agg gaa gac ttg gtg gta gcc ccc cgc agc atc aca ctg aag    632
Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile Thr Leu Lys
180             185             190             195

gag gca aat gaa att ctg cag cgc agc aag aag gga aag ttg ccc att    680
Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys Leu Pro Ile
            200             205             210

gta aat gaa gat gat gag ctt gtg gcc atc att gcc cgg aca gac ctg    728
Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg Thr Asp Leu
            215             220             225

aag aag aat cgg gac tac cca cta gcc tcc aaa gat gcc aag aaa cag    776
Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala Lys Lys Gln
        230             235             240

ctg ctg tgt ggg gca gcc att ggc act cat gag gat gac aag tat agg    824
Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp Lys Tyr Arg
        245             250             255

ctg gac ttg ctc gcc cag gct ggt gtg gat gta gtg gtt ttg gac tct    872
Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu Asp Ser
260             265             270             275

tcc cgg gga aat tcc atc ttc cag atc aat atg atc aag tac atc aaa    920
Ser Arg Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys Tyr Ile Lys
                280             285             290

gac aaa tac cct aat ctc caa gtc att gga ggc aat gtg gtc act gct    968
Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val Thr Ala
            295             300             305

gcc cag gcc aag aac ctc att gat gca ggt gtg gat gcc ctg cgg gtg    1016
Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu Arg Val
        310             315             320

ggc atg gga agt ggc tcc atc tgc att acg cag gaa gtg ctg gcc tgt    1064
Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala Cys
        325             330             335

ggg cgg ccc caa gca aca gca gtg tac aag gtg tca gag tat gca cgg    1112
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Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu Tyr Ala Arg
340             345             350             355

cgc ttt ggt gtt ccg gtc att gct gat gga gga atc caa aat gtg ggt    1160
Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn Val Gly
                360             365             370

cat att gcg aaa gcc ttg gcc ctt ggg gcc tcc aca gtc atg atg ggc    1208
His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met Met Gly
                375             380             385

tct ctc ctg gct gcc acc act gag gcc cct ggt gaa tac ttc ttt tcc    1256
Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr Phe Phe Ser
            390             395             400

gat ggg atc cgg cta aag aaa tat cgc ggt atg ggt tct ctc gat gcc    1304
Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser Leu Asp Ala
        405             410             415

atg gac aag cac ctc agc agc cag aac aga tat ttc agt gaa gct gac    1352
Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu Ala Asp
420             425             430             435

aaa atc aaa gtg gcc cag gga gtg tct ggt gct gtg cag gac aaa ggg    1400
Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp Lys Gly
                440             445             450

tca atc cac aaa ttt gtc cct tac ctg att act ggc atc caa cac tca    1448
Ser Ile His Lys Phe Val Pro Tyr Leu Ile Thr Gly Ile Gln His Ser
                455             460             465

tgc cag gac att ggt gcc aag agc ttg acc caa gtc cga gcc atg atg    1496
Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala Met Met
            470             475             480

tac tct ggg gag ctt aag ttt gag aag aga acg tcc tca gcc cag gtg    1544
Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala Gln Val
            485             490             495

gaa ggt ggc gtc cat agc ctc cat tcg tat gag aag cgg ctt ttc        1589
Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu Phe
500             505             510

tgaaaaggga tccagcacac ctcctcggtt tttttttcaa taaaagttta gaaagacccg    1649
aattc                                                              1654
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<210> 10
<211> 514
<212> PRT
<213> Homo sapien

<400> 10
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Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
1               5               10              15
Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
            20              25              30
Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
            35              40              45
Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
        50              55              60
Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
65              70              75              80
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```
Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
                85                      90                      95
Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
            100                     105                 110
Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
            115                 120                 125
Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
            130             135             140
Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
145             150                     155                     160
Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu
                165                 170                 175
Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile
            180                 185                 190
Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
        195                 200                 205
Leu Pro Ile Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg
    210                 215                 220
Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
225                 230                 235                 240
Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
                245                 250                 255
Lys Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val
        260                 265                 270
Leu Asp Ser Ser Arg Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
        275                 280                 285
Tyr Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val
290                 295                 300
Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
305                 310                 315                 320
Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val
            325                 330                 335
Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu
            340                 345                 350
Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
        355                 360                 365
Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
    370                 375                 380
Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
385                 390                 395                 400
Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
            405                 410                 415
Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser
            420                 425                 430
Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
        435                 440                 445
Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Thr Gly Ile
    450                 455                 460
Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg
465                 470                 475                 480
Ala Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser
                485                 490                 495
Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg
            500                 505                 510
Leu Phe
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<210> 11
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<213> Homo sapien

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<220>
<221> mutation
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<223> T to C

<221> mutation
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<221> CDS
<222> (48)...(1589)
<223> Phe456Ser/Asp470Gly Human IMPDH II mutant

<300>
<301> Farazi et al.
<303> J. Biol. Chem. (1997)
<304> 272
<305> 2
<306> 961-965


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gaattcgggc ggtcctcgga gacacgcggc ggtgtcctgt gttggcc atg gcc gac        56
                                                    Met Ala Asp
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tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga ctc aca       104
Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr
     5                   10                  15

gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt       152
Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe
 20          ·          25                  30                  35

ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg       200
Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu
                 40                  45                  50

act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg gtt tcc       248
Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu Val Ser
             55                  60                  65

tct ccc atg gac aca gtc aca gag gct ggg atg gcc ata gca atg gcg       296
Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile Ala Met Ala
         70                  75                  80

ctt aca ggc ggt att ggc ttc atc cac cac aac tgt aca cct gaa ttc       344
Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro Glu Phe
     85                  90                  95

cag gcc aat gaa gtt cgg aaa gtg aag aaa tat gaa cag gga ttc atc       392
Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln Gly Phe Ile
100                 105                 110                 115

aca gac cct gtg gtc ctc agc ccc aag gat cgc gtg cgg gat gtt ttt       440
Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg Asp Val Phe
                120                 125                 130

gag gcc aag gcc cgg cat ggt ttc tgc ggt atc cca atc aca gac aca       488
Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile Thr Asp Thr
             135                 140                 145

ggc cgg atg ggg agc cgc ttg gtg ggc atc atc tcc tcc agg gac att       536
```

```
Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser Arg Asp Ile
        150                 155             160
```

```
gat ttt ctc aaa gag gag gaa cat gac tgt ttc ttg gaa gag ata atg    584
Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu Glu Ile Met
    165                 170                 175
```

```
aca aag agg gaa gac ttg gtg gta gcc ccc cgc agc atc aca ctg aag    632
Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile Thr Leu Lys
180                 185                 190                 195
```

```
gag gca aat gaa att ctg cag cgc agc aag aag gga aag ttg ccc att    680
Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys Leu Pro Ile
                200                 205                 210
```

```
gta aat gaa gat gat gag ctt gtg gcc atc att gcc cgg aca gac ctg    728
Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg Thr Asp Leu
                215                 220                 225
```

```
aag aag aat cgg gac tac cca cta gcc tcc aaa gat gcc aag aaa cag    776
Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala Lys Lys Gln
            230                 235                 240
```

```
ctg ctg tgt ggg gca gcc att ggc act cat gag gat gac aag tat agg    824
Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp Lys Tyr Arg
    245                 250                 255
```

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ctg gac ttg ctc gcc cag gct ggt gtg gat gta gtg gtt ttg gac tct    872
Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu Asp Ser
260                 265                 270                 275
```

```
tcc cag gga aat tcc atc ttc cag atc aat atg atc aag tac atc aaa    920
Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys Tyr Ile Lys
                280                 285                 290
```

```
gac aaa tac cct aat ctc caa gtc att gga ggc aat gtg gtc act gct    968
Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val Thr Ala
                295                 300                 305
```

```
gcc cag gcc aag aac ctc att gat gca ggt gtg gat gcc ctg cgg gtg   1016
Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu Arg Val
        310                 315                 320
```

```
ggc atg gga agt ggc tcc atc tgc att acg cag gaa gtg ctg gcc tgt   1064
Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala Cys
        325                 330                 335
```

```
ggg cgg ccc caa gca aca gca gtg tac aag gtg tca gag tat gca cgg   1112
Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu Tyr Ala Arg
340                 345                 350                 355
```

```
cgc ttt ggt gtt ccg gtc att gct gat gga gga atc caa aat gtg ggt   1160
Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn Val Gly
                360                 365                 370
```

```
cat att gcg aaa gcc ttg gcc ctt ggg gcc tcc aca gtc atg atg ggc   1208
His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met Met Gly
            375                 380                 385
```

```
tct ctc ctg gct gcc acc act gag gcc cct ggt gaa tac ttc ttt tcc   1256
Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr Phe Phe Ser
        390                 395                 400
```

```
gat ggg atc cgg cta aag aaa tat cgc ggt atg ggt tct ctc gat gcc     1304
Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser Leu Asp Ala
    405             410             415

atg gac aag cac ctc agc agc cag aac aga tat ttc agt gaa gct gac     1352
Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu Ala Asp
420             425             430                 435

aaa atc aaa gtg gcc cag gga gtg tct ggt gct gtg cag gac aaa ggg     1400
Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp Lys Gly
                440             445             450

tca atc cac aaa tct gtc cct tac ctg att gct ggc atc caa cac tca     1448
Ser Ile His Lys Ser Val Pro Tyr Leu Ile Ala Gly Ile Gln His Ser
            455             460             465

tgc cag ggc att ggt gcc aag agc ttg acc caa gtc cga gcc atg atg     1496
Cys Gln Gly Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala Met Met
        470             475             480

tac tct ggg gag ctt aag ttt gag aag aga acg tcc tca gcc cag gtg     1544
Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala Gln Val
    485             490             495

gaa ggt ggc gtc cat agc ctc cat tcg tat gag aag cgg ctt ttc         1589
Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu Phe
500             505             510

tgaaaaggga tccagcacac ctcctcggtt ttttttttcaa taaaagttta gaaagacccg   1649
aattc                                                               1654
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<210> 12
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<213> Homo sapien

<400> 12

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 1               5                  10                  15
Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
            20                  25                  30
Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
            35                  40                  45
Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
        50                  55                  60
Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
65                  70                  75                  80
Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
                85                  90                  95
Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
            100                 105                 110
Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
        115                 120                 125
Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
        130                 135                 140
Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
145                 150                 155                 160
Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu
                165                 170                 175
Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile
            180                 185                 190
```

```
Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
        195                 200                 205
Leu Pro Ile Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg
    210                 215                 220
Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
225                 230                 235                 240
Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
                245                 250                 255
Lys Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val
            260                 265                 270
Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
        275                 280                 285
Tyr Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val
    290                 295                 300
Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
305                 310                 315                 320
Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val
                325                 330                 335
Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu
            340                 345                 350
Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
    355                 360                 365
Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
    370                 375                 380
Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
385                 390                 395                 400
Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
                405                 410                 415
Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser
            420                 425                 430
Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
            435                 440                 445
Asp Lys Gly Ser Ile His Lys Ser Val Pro Tyr Leu Ile Ala Gly Ile
    450                 455                 460
Gln His Ser Cys Gln Gly Ile Gly Ala Lys Ser Leu Thr Gln Val Arg
465                 470                 475                 480
Ala Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser
            485                 490                 495
Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg
        500                 505                 510
Leu Phe
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<210> 13
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<213> Tritrichomonas foetus

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<223> T. foetus IMPDH Type II

<300>
<301> Beck,J.T., Zhao,S. and Wang,C.C.
<302> Cloning, sequencing, and structural analysis of th
<303> Exp. Parasitol. (1994)
<304> 78
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<306> 101-112

<400> 13

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ttcacatttc atctcacata gcttttttat ttttttcatt gtaagtccaa acaa atg      117
                                                             Met
                                                              1

gca aaa tac tac aac gaa cca tgc cac acc ttt aac gaa tat ctc ctc      165
Ala Lys Tyr Tyr Asn Glu Pro Cys His Thr Phe Asn Glu Tyr Leu Leu
            5                   10                  15

att cca gga ctc tca aca gtc gac tgc att cca tcc aac gtt aac tta      213
Ile Pro Gly Leu Ser Thr Val Asp Cys Ile Pro Ser Asn Val Asn Leu
        20                  25                  30

tct acc cca ctc gtc aag ttc caa aag ggg caa caa agt gag atc aat      261
Ser Thr Pro Leu Val Lys Phe Gln Lys Gly Gln Gln Ser Glu Ile Asn
        35                  40                  45

tta aag atc ccc ctt gtt tct gcc atc atg caa tct gtc tca gga gaa      309
Leu Lys Ile Pro Leu Val Ser Ala Ile Met Gln Ser Val Ser Gly Glu
50                  55                  60                  65

aag atg gct atc gca ttg gca cga gaa ggt ggt att tca ttc att ttc      357
Lys Met Ala Ile Ala Leu Ala Arg Glu Gly Gly Ile Ser Phe Ile Phe
                70                  75                  80

gga tct caa tca att gaa agc caa gca gcc atg gtc cat gct gtc aaa      405
Gly Ser Gln Ser Ile Glu Ser Gln Ala Ala Met Val His Ala Val Lys
            85                  90                  95

aat ttc aaa gcc ggc ttt gtc gtc tca gat tca aac gtt aaa cca gat      453
Asn Phe Lys Ala Gly Phe Val Val Ser Asp Ser Asn Val Lys Pro Asp
        100                 105                 110

caa aca ttt gct gat gtt tta gca att tct caa cga aca acc cac aac      501
Gln Thr Phe Ala Asp Val Leu Ala Ile Ser Gln Arg Thr Thr His Asn
        115                 120                 125

act gtc gct gtc aca gac gat gga act cca cat gga gtt tta ctt ggt      549
Thr Val Ala Val Thr Asp Asp Gly Thr Pro His Gly Val Leu Leu Gly
130                 135                 140                 145

ttg gtc act caa cgc gat tat cca atc gat ctt acc cag acc gaa aca      597
Leu Val Thr Gln Arg Asp Tyr Pro Ile Asp Leu Thr Gln Thr Glu Thr
                150                 155                 160

aag gtt tcc gac atg atg aca cca ttc agc aag ctc gtt aca gcc cat      645
Lys Val Ser Asp Met Met Thr Pro Phe Ser Lys Leu Val Thr Ala His
                165                 170                 175

cag gac aca aaa ctt tca gaa gcc aac aaa att att tgg gag aag aaa      693
Gln Asp Thr Lys Leu Ser Glu Ala Asn Lys Ile Ile Trp Glu Lys Lys
                180                 185                 190

tta aat gct ctt cct atc att gat gac gat caa cat ctt cgt tat atc      741
Leu Asn Ala Leu Pro Ile Ile Asp Asp Asp Gln His Leu Arg Tyr Ile
                195                 200                 205

gtt ttc cgc aaa gat tat gac aga tcg caa gtc tgt cac aac gaa ctc      789
Val Phe Arg Lys Asp Tyr Asp Arg Ser Gln Val Cys His Asn Glu Leu
210                 215                 220                 225

gtc gat tcg caa aaa cgc tat ttg gtc gga gca gga att aac aca cgc      837
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Val Asp Ser Gln Lys Arg Tyr Leu Val Gly Ala Gly Ile Asn Thr Arg
            230             235                 240

gac ttc aga gaa cgc gtt cca gca ctt gtc gaa gcc ggc gct gat gtc   885
Asp Phe Arg Glu Arg Val Pro Ala Leu Val Glu Ala Gly Ala Asp Val
            245             250                 255

ctt tgc att gat tcc agc gac ggc ttc tca gaa tgg cag aaa att aca   933
Leu Cys Ile Asp Ser Ser Asp Gly Phe Ser Glu Trp Gln Lys Ile Thr
            260             265                 270

atc ggc tgg att cgc gag aaa tac ggc gat aaa gtt aaa gtt ggt gcg   981
Ile Gly Trp Ile Arg Glu Lys Tyr Gly Asp Lys Val Lys Val Gly Ala
            275             280                 285

gga aac att gtt gac ggt gaa gga ttc cgc tat ttg gcc gac gct gga  1029
Gly Asn Ile Val Asp Gly Glu Gly Phe Arg Tyr Leu Ala Asp Ala Gly
290             295                 300             305

gct gat ttc atc aag att gga att ggc ggt gga tca att tgc atc aca  1077
Ala Asp Phe Ile Lys Ile Gly Ile Gly Gly Gly Ser Ile Cys Ile Thr
            310             315                 320

cgc gag cag aaa ggt atc ggc cga ggc caa gct act gcc gtc att gat  1125
Arg Glu Gln Lys Gly Ile Gly Arg Gly Gln Ala Thr Ala Val Ile Asp
            325             330                 335

gtt gtt gca gag cgt aac aaa tac ttc gaa gag acc gga att tat atc  1173
Val Val Ala Glu Arg Asn Lys Tyr Phe Glu Glu Thr Gly Ile Tyr Ile
            340             345                 350

cct gtt tgc tct gat ggt gga att gtt tat gat tat cac atg aca ctt  1221
Pro Val Cys Ser Asp Gly Gly Ile Val Tyr Asp Tyr His Met Thr Leu
            355             360                 365

gct ctt gca atg ggc gca gat ttc atc atg ctt ggc agg tac ttc gcc  1269
Ala Leu Ala Met Gly Ala Asp Phe Ile Met Leu Gly Arg Tyr Phe Ala
370             375                 380             385

cgt ttt gag gag tca cca aca aga aaa gtg aca att aat gga agc gtt  1317
Arg Phe Glu Glu Ser Pro Thr Arg Lys Val Thr Ile Asn Gly Ser Val
            390             395                 400

atg aag gag tac tgg gga gaa ggc tct tcg cgc gct agg aac tgg cag  1365
Met Lys Glu Tyr Trp Gly Glu Gly Ser Ser Arg Ala Arg Asn Trp Gln
            405             410                 415

cgc tat gac ctt gga ggt aag cag aag ctt tcc ttt gaa gag gga gtc  1413
Arg Tyr Asp Leu Gly Gly Lys Gln Lys Leu Ser Phe Glu Glu Gly Val
            420             425                 430

gat tct tac gtc cca tac gct gga aag ttg aag gac aac gtg gag gca  1461
Asp Ser Tyr Val Pro Tyr Ala Gly Lys Leu Lys Asp Asn Val Glu Ala
            435             440                 445

tcc ttg aac aag gta aaa tca acg atg tgc aac tgt gga gcg ctc aca  1509
Ser Leu Asn Lys Val Lys Ser Thr Met Cys Asn Cys Gly Ala Leu Thr
450             455                 460             465

atc ccg cag ctc cag agc aag gca aag atc aca ctt gta tca tca gtt  1557
Ile Pro Gln Leu Gln Ser Lys Ala Lys Ile Thr Leu Val Ser Ser Val
            470             475                 480
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tca att gtc gaa gga ggc gca cac gat gtt att gtt aag gac agg att      1605
Ser Ile Val Glu Gly Gly Ala His Asp Val Ile Val Lys Asp Arg Ile
            485                 490                 495

aac gac tat cac cca aaa taaatatatt gttttatact ttatgtttgt            1653
Asn Asp Tyr His Pro Lys
            500

taaattatac ctatttactt ctcttgtttt tatgtctttt gattcttcca tgtctttgaa   1713
ttcttccatg tctttttgatt cttttttccca catggtgcat gtgttgaatt attcaaaacc  1773
cttttccttt gtaacttgtc attaattggc attttcggag tgaactagtt aattattttt   1833
ccaatgatat ttattatagt cttttttgtgt attgatgtct tactttactg atagtgatta  1893
ggtcaatact ctattatgga gtctgactcg cgttactcta tctatattaa ctataacaca   1953
tagcttagtc tacactgcgt agctcttgtt acttgacatg a                       1994
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<210> 14
<211> 503
<212> PRT
<213> Tritrichomonas foetus

<400> 14

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Met Ala Lys Tyr Tyr Asn Glu Pro Cys His Thr Phe Asn Glu Tyr Leu
1               5                   10                  15
Leu Ile Pro Gly Leu Ser Thr Val Asp Cys Ile Pro Ser Asn Val Asn
            20                  25                  30
Leu Ser Thr Pro Leu Val Lys Phe Gln Lys Gly Gln Gln Ser Glu Ile
            35                  40                  45
Asn Leu Lys Ile Pro Leu Val Ser Ala Ile Met Gln Ser Val Ser Gly
    50                  55                  60
Glu Lys Met Ala Ile Ala Leu Ala Arg Glu Gly Gly Ile Ser Phe Ile
65                  70                  75                  80
Phe Gly Ser Gln Ser Ile Glu Ser Gln Ala Ala Met Val His Ala Val
                85                  90                  95
Lys Asn Phe Lys Ala Gly Phe Val Val Ser Asp Ser Asn Val Lys Pro
                100                 105                 110
Asp Gln Thr Phe Ala Asp Val Leu Ala Ile Ser Gln Arg Thr Thr His
            115                 120                 125
Asn Thr Val Ala Val Thr Asp Asp Gly Thr Pro His Gly Val Leu Leu
    130                 135                 140
Gly Leu Val Thr Gln Arg Asp Tyr Pro Ile Asp Leu Thr Gln Thr Glu
145                 150                 155                 160
Thr Lys Val Ser Asp Met Met Thr Pro Phe Ser Lys Leu Val Thr Ala
                165                 170                 175
His Gln Asp Thr Lys Leu Ser Glu Ala Asn Lys Ile Ile Trp Glu Lys
            180                 185                 190
Lys Leu Asn Ala Leu Pro Ile Ile Asp Asp Asp Gln His Leu Arg Tyr
    195                 200                 205
Ile Val Phe Arg Lys Asp Tyr Asp Arg Ser Gln Val Cys His Asn Glu
    210                 215                 220
Leu Val Asp Ser Gln Lys Arg Tyr Leu Val Gly Ala Gly Ile Asn Thr
225                 230                 235                 240
Arg Asp Phe Arg Glu Arg Val Pro Ala Leu Val Glu Ala Gly Ala Asp
                245                 250                 255
Val Leu Cys Ile Asp Ser Ser Asp Gly Phe Ser Glu Trp Gln Lys Ile
            260                 265                 270
Thr Ile Gly Trp Ile Arg Glu Lys Tyr Gly Asp Lys Val Lys Val Gly
            275                 280                 285
Ala Gly Asn Ile Val Asp Gly Glu Gly Phe Arg Tyr Leu Ala Asp Ala
    290                 295                 300
Gly Ala Asp Phe Ile Lys Ile Gly Ile Gly Gly Gly Ser Ile Cys Ile
305                 310                 315                 320
```

```
Thr Arg Glu Gln Lys Gly Ile Gly Arg Gly Gln Ala Thr Ala Val Ile
                325                 330                 335
Asp Val Val Ala Glu Arg Asn Lys Tyr Phe Glu Glu Thr Gly Ile Tyr
            340                 345                 350
Ile Pro Val Cys Ser Asp Gly Gly Ile Val Tyr Asp Tyr His Met Thr
            355                 360                 365
Leu Ala Leu Ala Met Gly Ala Asp Phe Ile Met Leu Gly Arg Tyr Phe
        370                 375                 380
Ala Arg Phe Glu Glu Ser Pro Thr Arg Lys Val Thr Ile Asn Gly Ser
385                 390                 395                 400
Val Met Lys Glu Tyr Trp Gly Glu Gly Ser Ser Arg Ala Arg Asn Trp
                405                 410                 415
Gln Arg Tyr Asp Leu Gly Gly Lys Gln Lys Leu Ser Phe Glu Glu Gly
            420                 425                 430
Val Asp Ser Tyr Val Pro Tyr Ala Gly Lys Leu Lys Asp Asn Val Glu
            435                 440                 445
Ala Ser Leu Asn Lys Val Lys Ser Thr Met Cys Asn Cys Gly Ala Leu
        450                 455                 460
Thr Ile Pro Gln Leu Gln Ser Lys Ala Lys Ile Thr Leu Val Ser Ser
465                 470                 475                 480
Val Ser Ile Val Glu Gly Gly Ala His Asp Val Ile Val Lys Asp Arg
                485                 490                 495
Ile Asn Asp Tyr His Pro Lys
                500
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<210> 15
<211> 1560
<212> DNA
<213> Aspergillus nidulans

<220>
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<222> (1)...(1560)
<223> Aspergillus nidulans wild type DHODH cDNA

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atg gct acg aat tct ttc cga aaa ctc act ttt tca gga gcc tcc cgt          48
Met Ala Thr Asn Ser Phe Arg Lys Leu Thr Phe Ser Gly Ala Ser Arg
1               5                   10                  15


ctg ggt ggt tgt cgc cgt ctc cca cta acc tgc aga caa ctt cga ttc          96
Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe
            20                  25                  30


gcc tcc gac agc gga gcc gca gcg gca act aca aaa gca acg gcc gaa         144
Ala Ser Asp Ser Gly Ala Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu
        35                  40                  45


tca gca gcc gag tca gct agt ata aac gtc aaa gag gca ccc aaa aag         192
Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys
    50                  55                  60


gcc gga cgg ggc ctg cgg cgc acg gtc ctg gga acg tcg ttg gcg ctg         240
Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu
65                  70                  75                  80


acg ctg ctg gtt gga tat gtc tac ggg acg gac acc cgg gcg agt gtg         288
Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val
                85                  90                  95


cat cgg tac ggt gtt gtg ccg ctg att aga gca ttg tat cct gat gcg         336
His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala
```

```
                    100                     105                     110
gaa gat gcg cat cat att ggt gtc gat act tta aag atg ctg tat aag    384
Glu Asp Ala His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys
        115                 120                 125

tat ggt ctg cat cca agg gaa cgg ggg gat ccg gat gga gat ggg gcg    432
Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala
    130                 135                 140

ctg gcg aca gag gtc ttt ggg tat aca ctg tca aac cca att ggc ata    480
Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile
145                 150                 155                 160

tcg ggc ggc ctg gac aag cat gct gag atc cct gat ccg ctg ttc gcg    528
Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala
                165                 170                 175

atc ggt cct gcc att gtc gaa gtc ggg ggt acg aca ccc tta cca cag    576
Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln
                180                 185                 190

gat ggt aac ccg cgt cct cgc gta ttc cga ctt cca tca cag aga gcg    624
Asp Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Ser Gln Arg Ala
            195                 200                 205

atg ata aac cgg tac ggc ctc aac tcc aaa ggc gca gat cac atg gca    672
Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala
    210                 215                 220

gct atc ttg gag caa cga gta cgc gat ttt gcc tac gca aac gga ttt    720
Ala Ile Leu Glu Gln Arg Val Arg Asp Phe Ala Tyr Ala Asn Gly Phe
225                 230                 235                 240

ggg gca tac gat gcg gct aag cag cgt gta ttg gac ggc gaa gct ggt    768
Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly
                245                 250                 255

gtg cca cca ggt agt ctt cag cct ggt aag ctt tta gct gtc caa gtg    816
Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val
                260                 265                 270

gca aag aac aag gcc act cct gac ggc gac att gaa gcc atc aag cgc    864
Ala Lys Asn Lys Ala Thr Pro Asp Gly Asp Ile Glu Ala Ile Lys Arg
            275                 280                 285

gac tat gtg tat tgc gtg gac cgt gtg gcc aaa tac gct gat att ctt    912
Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu
    290                 295                 300

gtt gtg aat gta tcg agc ccc aac aca ccc ggt ctc cgt gac ctt caa    960
Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln
305                 310                 315                 320

gcc act gcc ccg ctc aca gct atc ttg agt gct gtc gtt ggc gcg gca   1008
Ala Thr Ala Pro Leu Thr Ala Ile Leu Ser Ala Val Val Gly Ala Ala
                325                 330                 335

aag agc gtg aac cgc aag acc aaa cca tat gtt atg gtc aag gtc agt   1056
Lys Ser Val Asn Arg Lys Thr Lys Pro Tyr Val Met Val Lys Val Ser
            340                 345                 350
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ccg gat gaa gac tca gat gaa caa gtc tct ggt atc tgc gac gcc gtc     1104
Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val
        355                 360                 365

cga gca tcc ggt gtc gac gga gtg att gtc gga aac aca aca aac cgt     1152
Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg
    370                 375                 380

cgc ccc gac cct ata ccc caa ggt tac act ctt ccg gcc aag gag cag     1200
Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln
385                 390                 395                 400

gca acg ttg aaa gaa acc ggc ggg tat tca ggt cca cag ctg ttc gat     1248
Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp
            405                 410                 415

cgc aca gtg gcc ctt gtg gct cgg tac cgc tcc atg ctg gat gcg gag     1296
Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu
            420                 425                 430

tcg gaa acg gcc gga tcc gcc aag gat tca gca gcg acc ata gcg caa     1344
Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln
            435                 440                 445

aca gag cca ggc tcg gaa aac gtt cct cct gtg gaa gcg cca agc gga     1392
Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly
    450                 455                 460

ctg ccg cgc aaa gtt atc ttc gct tcg ggt ggt atc acc aac ggg aag     1440
Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys
465                 470                 475                 480

cag gct cac gct gtt tta gac aca ggg gca tct gtt gcc atg atg tac     1488
Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr
            485                 490                 495

acc ggt gtg gtc tat ggt ggc gtc ggc act gtc act cga gtg aag caa     1536
Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln
            500                 505                 510

gaa ctt cga acg gcg aaa aag gag                                     1560
Glu Leu Arg Thr Ala Lys Lys Glu
        515                 520
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<210> 16
<211> 520
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<213> Aspergillus nidulans

<400> 16
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1               5                   10                  15
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            20                  25                  30
Ala Ser Asp Ser Gly Ala Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu
        35                  40                  45
Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys
    50                  55                  60
Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu
65                  70                  75                  80
Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val
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                    85                      90                      95
His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala
                100                     105                     110
Glu Asp Ala His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys
            115                     120                     125
Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala
        130                     135                     140
Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile
145                     150                     155                     160
Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala
                165                     170                     175
Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln
                180                     185                     190
Asp Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Ser Gln Arg Ala
            195                     200                     205
Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala
    210                     215                     220
Ala Ile Leu Glu Gln Arg Val Arg Asp Phe Ala Tyr Ala Asn Gly Phe
225                     230                     235                     240
Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly
                245                     250                     255
Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val
            260                     265                     270
Ala Lys Asn Lys Ala Thr Pro Asp Gly Asp Ile Glu Ala Ile Lys Arg
        275                     280                     285
Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu
    290                     295                     300
Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln
305                     310                     315                     320
Ala Thr Ala Pro Leu Thr Ala Ile Leu Ser Ala Val Val Gly Ala Ala
                325                     330                     335
Lys Ser Val Asn Arg Lys Thr Lys Pro Tyr Val Met Val Lys Val Ser
            340                     345                     350
Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val
            355                     360                     365
Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg
    370                     375                     380
Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln
385                     390                     395                     400
Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp
                405                     410                     415
Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu
            420                     425                     430
Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln
            435                     440                     445
Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly
        450                     455                     460
Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys
465                     470                     475                     480
Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr
            485                     490                     495
Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln
        500                     505                     510
Glu Leu Arg Thr Ala Lys Lys Glu
        515                     520
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<213> Homo sapien

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<223> Human wild-type IMPDH type I

<300>
<301> Natsumeda et al.
<302> Two Distinct cDNAs for Human IMP Dehydrogenase
<303> J. Biol. Chem. (1990)
<304> 265
<305> 9
<306> 5292-5295

<400> 17
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tcggaagggg ccaggagaca ctggaaggtc cggacggcag ggaagggggac ggggttcttt      60
ccagtcccac ccgtgtaggg acacctctcc ccctcatccc ccgatgtacc ctcgctgaat     120
ctgggatggg agagacgaac cgagtctagg catctgcgta gcagcgccgg ggagagcggg     180
gagcccaggc ggagcccagt cgactcccgg attcccctgc cccgcccccg gcacgaggcc     240
ccgccccggc gccccgcccc tcctcgggac tcgaccgggc tgcgctcact gcccagccgg     300
ggccccggga gcctccaggc tcgcccgccc tgagctgcgg cctccgcatg gagggccact     360
cactccacca ccgctgcagg gaggcggacg gcgctgttcc ggagcccgga gcccggcaac     420
acccgggaca cgagacggcg gcgcagggct acagcgcccg actgctgcag gccggctacg     480
agcccgagag ccctagattg gacctcgcta cacacccgac gacacccgt tcagaactat     540
cttcagtggt cttactggca ggtgttggtg ccagatgga tcgccttcgc agggctagcc     600
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atg gcg gac tac ctg atc agc ggc ggc acc ggc tac gtg ccc gag gat      648
Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Gly Tyr Val Pro Glu Asp
 1               5                  10                  15

ggg ctc acc gcg cag cag ctc ttc gcc agc gcc gac gac ctc acc tac      696
Gly Leu Thr Ala Gln Gln Leu Phe Ala Ser Ala Asp Asp Leu Thr Tyr
            20              25                  30

aac gac ttc ctg att ctc cca gga ttc ata gac ttc ata gct gat gag      744
Asn Asp Phe Leu Ile Leu Pro Gly Phe Ile Asp Phe Ile Ala Asp Glu
        35                  40                  45

gtg gac ctg acc tca gcc ctg acc cgg aag atc acg ctg aag acg cca      792
Val Asp Leu Thr Ser Ala Leu Thr Arg Lys Ile Thr Leu Lys Thr Pro
    50                  55                  60

ctc atc tcc tcc ccc atg gac act gtg aca gag gct gac atg gcc att      840
Leu Ile Ser Ser Pro Met Asp Thr Val Thr Glu Ala Asp Met Ala Ile
65                  70                  75                  80

gcc atg gct ctg atg gga ggt att ggg ttc att cac cac aac tgc acc      888
Ala Met Ala Leu Met Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
                85                  90                  95

cca gag ttc cag gcc aat gaa gta cgc aag gtc aag aac ttt gaa cag      936
Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Asn Phe Glu Gln
            100                 105                 110

ggc ttc atc acg gac cct gtg gtg ctg agc ccc tcg cac act gtg ggc      984
Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Ser His Thr Val Gly
        115                 120                 125

gat gtg ctg gag gcc aag atg cgg cat ggc ttc tct ggc atc ccc atc     1032
Asp Val Leu Glu Ala Lys Met Arg His Gly Phe Ser Gly Ile Pro Ile
        130                 135                 140

act gag acg ggc acc atg ggc agc aag ctg gtg ggc atc gtc acc tcc     1080
Thr Glu Thr Gly Thr Met Gly Ser Lys Leu Val Gly Ile Val Thr Ser
145                 150                 155                 160
```

```
cga gac atc gac ttt ctt gct gag aag gac cac acc acc ctc ctc agt    1128
Arg Asp Ile Asp Phe Leu Ala Glu Lys Asp His Thr Thr Leu Leu Ser
            165                 170                 175

gag gtg atg acg cca agg att gaa ctg gtg gtg gct cca gca ggt gtg    1176
Glu Val Met Thr Pro Arg Ile Glu Leu Val Val Ala Pro Ala Gly Val
            180                 185                 190

acg ttg aaa gag gca aat gag atc ctg cag cgt agc aag aaa ggg aag    1224
Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
            195                 200                 205

ctg cct atc gtc aat gat tgc gat gag ctg gtg gcc atc atc gcc cgc    1272
Leu Pro Ile Val Asn Asp Cys Asp Glu Leu Val Ala Ile Ile Ala Arg
        210                 215                 220

acc gac ctg aag aag aat cga gac tac cct ctg gcc tcc aag gat tcc    1320
Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ser
225                 230                 235                 240

cag aag cag ctg ctc tgt ggg gca gct gtg ggc acc cgt gag gat gac    1368
Gln Lys Gln Leu Leu Cys Gly Ala Ala Val Gly Thr Arg Glu Asp Asp
                245                 250                 255

aaa tac cgt ctg gac ctg ctg acc cag gcg ggg gtc gac gtc ata gtc    1416
Lys Tyr Arg Leu Asp Leu Leu Thr Gln Ala Gly Val Asp Val Ile Val
                260                 265                 270

ttc cac tcg tcc caa ggg aat tcg gtg tat cag atc gcc atg gtg cat    1464
Phe His Ser Ser Gln Gly Asn Ser Val Tyr Gln Ile Ala Met Val His
                275                 280                 285

tac atc aaa cag aag tac ccc cac ctc cag gtg att ggg ggg aac gtg    1512
Tyr Ile Lys Gln Lys Tyr Pro His Leu Gln Val Ile Gly Gly Asn Val
            290                 295                 300

gtg aca gca gcc cag gcc aag aac ctg att gat gct ggt gtg gac ggg    1560
Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Gly
305                 310                 315                 320

ctg cgc gtg ggc atg ggc tgc ggc tcc atc tgc atc acc cag gaa gtg    1608
Leu Arg Val Gly Met Gly Cys Gly Ser Ile Cys Ile Thr Gln Glu Val
                325                 330                 335

atg gcc tgt ggt cgg ccc cag ggc act gct gtg tac aag gtg gct gag    1656
Met Ala Cys Gly Arg Pro Gln Gly Thr Ala Val Tyr Lys Val Ala Glu
                340                 345                 350

tat gcc cgg cgc ttt ggt gtg ccc atc ata gcc gat ggc ggc atc cag    1704
Tyr Ala Arg Arg Phe Gly Val Pro Ile Ile Ala Asp Gly Gly Ile Gln
            355                 360                 365

acc gtg gga cac gtg gtc aag gcc ctg gcc ctt gga gcc tcc aca gtg    1752
Thr Val Gly His Val Val Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
            370                 375                 380

atg atg ggc tcc ctg ctg gcc gcc act acg gag gcc cct ggc gag tac    1800
Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
385                 390                 395                 400

ttc ttc tca gac ggg gtg cgg ctc aag aag tac cgg ggc atg ggc tca    1848
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Phe Phe Ser Asp Gly Val Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
            405                 410                 415

ctg gat ccc atg gag aag agc agc agc agc cag aaa cga tac ttc agc      1896
Leu Asp Pro Met Glu Lys Ser Ser Ser Ser Gln Lys Arg Tyr Phe Ser
            420                 425                 430

gag ggg gat aaa gtg aag atc gca cag ggt gtc tcg ggc tcc atc cag      1944
Glu Gly Asp Lys Val Lys Ile Ala Gln Gly Val Ser Gly Ser Ile Gln
            435                 440                 445

gac aaa gga tcc att cag aag ttc gtg ccc tac ctc ata gca ggc atc      1992
Asp Lys Gly Ser Ile Gln Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
        450                 455                 460

caa cac ggc tgc cag gat atc ggg gcc cgc agc ctg tct gtc ctt cgg      2040
Gln His Gly Cys Gln Asp Ile Gly Ala Arg Ser Leu Ser Val Leu Arg
465                 470                 475                 480

tcc atg atg tac tca gga gag ctc aag ttt gag aag cgg acc atg tcg      2088
Ser Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Met Ser
                485                 490                 495

ccc cag att gag ggt ggt gtc cat ggc ctg cac tct tac gaa aag cgg      2136
Pro Gln Ile Glu Gly Gly Val His Gly Leu His Ser Tyr Glu Lys Arg
            500                 505                 510

ctg tac tgaggacagc ggtggaggcc gaggtggtgg aggggatgca ccccagtgtc      2192
Leu Tyr


cacttttggg cacaggctcc ctccataact gagtggtcca cagatttgca ctacgggttc      2252
tccagctcct ttccaggcag agaggagggg aggtcctgag gggactgctg cccctcactc      2312
ggcatcccct gcagagtcag gactgctccc gggggccagg ctgccctggg aggccccctc      2372
cgagaccagc cagccaggct ctcaggacct gcgctgcctt aggatctttc ttgctgcagc      2432
ctgctccagc ctggcccccca ccccagggggc aggcggcccc tcctggcttc tcctgtaggg      2492
cacctccctg ccccctagcct cccagcaaat ggtgctctcc tggccctgct ctggcccttc      2552
ccgggccgtg cccctcagcc atgtggcact tctgagctcc tgacctaggc caaggggagg      2612
tctctgcccc cttccccggc cctgggctac ccttgggtcc tgctcctcag gccgctcccc      2672
tgtccctggc catgggtagg agactgccct ggtcatggcc gcctgcctgt cattcctgac      2732
tcaccaccgt ccccaggtga accattcctc ccttctcctc agctgcagtc gaaggcttta      2792
actttgcaca cttgggatca cagttgcgtc attgtgtatt aaatacttgg aataaatcaa      2852
gcaggt                                                                  2858
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<211> 514
<212> PRT
<213> Homo sapien

<400> 18
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Gly Leu Thr Ala Gln Gln Leu Phe Ala Ser Ala Asp Asp Leu Thr Tyr
            20                  25                  30
Asn Asp Phe Leu Ile Leu Pro Gly Phe Ile Asp Phe Ile Ala Asp Glu
            35                  40                  45
Val Asp Leu Thr Ser Ala Leu Thr Arg Lys Ile Thr Leu Lys Thr Pro
        50                  55                  60
Leu Ile Ser Ser Pro Met Asp Thr Val Thr Glu Ala Asp Met Ala Ile
65                  70                  75                  80
Ala Met Ala Leu Met Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
                85                  90                  95
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Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Asn Phe Glu Gln
            100                     105                 110
Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Ser His Thr Val Gly
        115                     120                 125
Asp Val Leu Glu Ala Lys Met Arg His Gly Phe Ser Gly Ile Pro Ile
    130                     135                 140
Thr Glu Thr Gly Thr Met Gly Ser Lys Leu Val Gly Ile Val Thr Ser
145                     150                     155             160
Arg Asp Ile Asp Phe Leu Ala Glu Lys Asp His Thr Thr Leu Leu Ser
                165                 170                     175
Glu Val Met Thr Pro Arg Ile Glu Leu Val Val Ala Pro Ala Gly Val
            180                     185                 190
Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
        195                     200                 205
Leu Pro Ile Val Asn Asp Cys Asp Glu Leu Val Ala Ile Ile Ala Arg
    210                     215                 220
Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ser
225                     230                     235             240
Gln Lys Gln Leu Leu Cys Gly Ala Ala Val Gly Thr Arg Glu Asp Asp
                245                 250                     255
Lys Tyr Arg Leu Asp Leu Leu Thr Gln Ala Gly Val Asp Val Ile Val
            260                     265                 270
Phe His Ser Ser Gln Gly Asn Ser Val Tyr Gln Ile Ala Met Val His
        275                     280                 285
Tyr Ile Lys Gln Lys Tyr Pro His Leu Gln Val Ile Gly Gly Asn Val
    290                     295                 300
Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Gly
305                     310                     315             320
Leu Arg Val Gly Met Gly Cys Gly Ser Ile Cys Ile Thr Gln Glu Val
                325                 330                     335
Met Ala Cys Gly Arg Pro Gln Gly Thr Ala Val Tyr Lys Val Ala Glu
            340                     345                 350
Tyr Ala Arg Arg Phe Gly Val Pro Ile Ile Ala Asp Gly Gly Ile Gln
        355                     360                 365
Thr Val Gly His Val Val Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
    370                     375                 380
Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
385                     390                     395             400
Phe Phe Ser Asp Gly Val Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
                405                 410                     415
Leu Asp Pro Met Glu Lys Ser Ser Ser Ser Gln Lys Arg Tyr Phe Ser
            420                     425                 430
Glu Gly Asp Lys Val Lys Ile Ala Gln Gly Val Ser Gly Ser Ile Gln
        435                     440                 445
Asp Lys Gly Ser Ile Gln Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
    450                     455                 460
Gln His Gly Cys Gln Asp Ile Gly Ala Arg Ser Leu Ser Val Leu Arg
465                     470                     475             480
Ser Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Met Ser
                485                 490                     495
Pro Gln Ile Glu Gly Gly Val His Gly Leu His Ser Tyr Glu Lys Arg
            500                     505                 510
Leu Tyr
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<210> 19
<211> 1496
<212> DNA
<213> Homo sapien

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<222> (0)...(1188)
<223> Human wild-type Dihydroorotate Dehydrogenase
      (DHODH) "PYRDH" cDNA clone

<300>
<301> Minet, M., Dufour, M-E., and Lacroute, F.
<302> Cloning and Sequencing of a Human cDNA coding for
<303> Gene (1992)
<304> 121
<306> 393-396

<400> 19
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aaa tta ccg tgg aga cac ctg caa aag cgg gcc cag gat gct gtg atc     48
Lys Leu Pro Trp Arg His Leu Gln Lys Arg Ala Gln Asp Ala Val Ile
 1               5                  10                  15

atc ctg ggg gga gga gga ctt ctc ttc gcc tcc tac ctg atg gcc acg     96
Ile Leu Gly Gly Gly Gly Leu Leu Phe Ala Ser Tyr Leu Met Ala Thr
                20                  25                  30

gga gat gag cgt ttc tat gct gaa cac ctg atg ccg act ctg cag ggg    144
Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr Leu Gln Gly
            35                  40                  45

ctg ctg gac ccg gag tca gcc cac aga ctg gct gtt cgc ttc acc tcc    192
Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg Phe Thr Ser
        50                  55                  60

ctg ggg ctc ctt cca cgg gcc aga ttt caa gac tct gac atg ctg gaa    240
Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met Leu Glu
65                  70                  75                  80

gtg aga gtt ctg ggc cat aaa ttc cga aat cca gta gga att gct gca    288
Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile Ala Ala
                85                  90                  95

gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat aag atg ggc    336
Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr Lys Met Gly
            100                 105                 110

ttt ggt ttt gtt gag ata gga agt gtg act cca aaa cct cag gaa gga    384
Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro Gln Glu Gly
            115                 120                 125

aac cct aga ccc aga gtc ttc cgc ctc cct gag gac caa gct gtc att    432
Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln Ala Val Ile
        130                 135                 140

aac agg tat gga ttt aac agt cac ggg ctt tca gtg gtg gaa cac agg    480
Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val Glu His Arg
145                 150                 155                 160

tta cgg gcc aga cag cag aag cag gcc aag ctc aca gaa gat gga ctg    528
Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu Asp Gly Leu
                165                 170                 175

cct ctg ggg gtc aac ttg ggg aag aac aag acc tca gtg gac gcc gcg    576
Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val Asp Ala Ala
            180                 185                 190

gag gac tac gca gaa ggg gtg cgc gta ctg ggc ccc ctg gcc gac tac    624
Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu Ala Asp Tyr
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              195                    200                    205

ctg gtg gtg aat gtg tcc agc ccc aac act gcc ggg ctg cgg agc ctt        672
Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu Arg Ser Leu
    210                    215                    220

cag gga aag gcc gag ctg cgc cgc ctg ctg acc aag gtg ctg cag gag        720
Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val Leu Gln Glu
225                    230                    235                    240

agg gat ggc ttg cgg aga gtg cac agg ccg gca gtc ctg gtg aag atc        768
Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu Val Lys Ile
                   245                    250                    255

gct cct gac ctc acc agc cag gat aag gag gac att gcc agt gtg gtc        816
Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala Ser Val Val
                   260                    265                    270

aaa gag ttg ggc atc gat ggg ctg att gtt acg aac acc acc gtg agt        864
Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr Thr Val Ser
                   275                    280                    285

cgc cct gcg ggc ctc cag ggt gcc ctg cgc tct gaa aca gga ggg ctg        912
Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr Gly Gly Leu
        290                    295                    300

agt ggg aag ccc ctc cgg gat tta tca act caa acc att cgg gag atg        960
Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile Arg Glu Met
305                    310                    315                    320

tat gca ctc acc caa ggc cga gtt ccc ata att ggg gtt ggt ggt gtg       1008
Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val Gly Gly Val
                   325                    330                    335

agc agc ggg cag gac gcg ctg gag aag atc cgg gca ggg gcc tcc ctg       1056
Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly Ala Ser Leu
                   340                    345                    350

gtg cag ctg tac acg gcc ctc acc ttc tgg ggg cca ccc gtt gtg ggc       1104
Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro Val Val Gly
                   355                    360                    365

aaa gtc aag cgg gaa ctg gag gcc ctt ctg aaa gag cag ggc ttt ggc       1152
Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln Gly Phe Gly
        370                    375                    380

gga gtc aca gat gcc att gga gca gat cat cgg agg tgaggacagc             1198
Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
385                    390                    395

gtctgacggg aagcctgatc tggaaccttc ccaaggactc aggcaagcct ttgtggctgg      1258
atcatgagag gagggactcc atcttgagcc atgtccccca gcctggcatg cgtgcactgt      1318
aaacgccaat cggggggtca ccaggatcaa ccgcaggctt tcttcagtcc cttggtcaga      1378
ccataaactg cattttttgat tctttgtgga ttcaaaccct aggatccatc agtcttgcaa     1438
ggacattgaa tattaggagg aaaaagtcat ggaaaaaata aagccattta gaacctgg        1496
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<210> 20
<211> 396
<212> PRT
<213> Homo Sapien

<400> 20

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Lys Leu Pro Trp Arg His Leu Gln Lys Arg Ala Gln Asp Ala Val Ile
1               5                   10                  15
Ile Leu Gly Gly Gly Gly Leu Leu Phe Ala Ser Tyr Leu Met Ala Thr
            20              25                  30
Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr Leu Gln Gly
        35              40                  45
Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg Phe Thr Ser
    50              55                  60
Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met Leu Glu
65              70              75                      80
Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile Ala Ala
            85                  90                  95
Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr Lys Met Gly
        100                 105                 110
Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro Gln Glu Gly
        115             120                 125
Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln Ala Val Ile
    130             135                 140
Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val Glu His Arg
145             150                 155                 160
Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu Asp Gly Leu
            165                 170                 175
Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val Asp Ala Ala
        180                 185                 190
Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu Ala Asp Tyr
        195                 200                 205
Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu Arg Ser Leu
    210             215                 220
Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val Leu Gln Glu
225             230                 235                 240
Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu Val Lys Ile
            245                 250                 255
Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala Ser Val Val
        260                 265                 270
Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr Thr Val Ser
    275                 280                 285
Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr Gly Gly Leu
    290             295                 300
Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile Arg Glu Met
305             310                 315                 320
Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val Gly Gly Val
            325                 330                 335
Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly Ala Ser Leu
            340                 345                 350
Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro Val Val Gly
        355                 360                 365
Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln Gly Phe Gly
        370             375                 380
Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
385                 390                 395
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<210> 21
<211> 1101
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (1)...(1101)
<223> DHODH Truncated 39 kDa Construct

<300>
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<301> Copeland, R.A., et al.
<302> Recombinant Human Dihydroorotate Dehydrogenase
<303> Arch. Biochem. Biophys. (1995)
<304> 323
<306> 79-86

<400> 21

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atg gcc acg gga gat gag cgt ttc tat gct gaa cac ctg atg ccg act    48
Met Ala Thr Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr
1               5                   10                  15

ctg cag ggg ctg ctg gac ccg gag tca gcc cac aga ctg gct gtt cgc    96
Leu Gln Gly Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg
            20                  25                  30

ttc acc tcc ctg ggg ctc ctt cca cgg gcc aga ttt caa gac tct gac   144
Phe Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp
            35                  40                  45

atg ctg gaa gtg aga gtt ctg ggc cat aaa ttc cga aat cca gta gga   192
Met Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly
    50                  55                  60

att gct gca gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat   240
Ile Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr
65                  70                  75                  80

aag atg ggc ttt ggt ttt gtt gag ata gga agt gtg act cca aaa cct   288
Lys Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro
                85                  90                  95

cag gaa gga aac cct aga ccc aga gtc ttc cgc ctc cct gag gac caa   336
Gln Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln
            100                 105                 110

gct gtc att aac agg tat gga ttt aac agt cac ggg ctt tca gtg gtg   384
Ala Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val
            115                 120                 125

gaa cac agg tta cgg gcc aga cag cag aag cag gcc aag ctc aca gaa   432
Glu His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu
            130                 135                 140

gat gga ctg cct ctg ggg gtc aac ttg ggg aag aac aag acc tca gtg   480
Asp Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val
145                 150                 155                 160

gac gcc gcg gag gac tac gca gaa ggg gtg cgc gta ctg ggc ccc ctg   528
Asp Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu
                165                 170                 175

gcc gac tac ctg gtg gtg aat gtg tcc agc ccc aac act gcc ggg ctg   576
Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu
            180                 185                 190

cgg agc ctt cag gga aag gcc gag ctg cgc cgc ctg ctg acc aag gtg   624
Arg Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val
            195                 200                 205

ctg cag gag agg gat ggc ttg cgg aga gtg cac agg ccg gca gtc ctg   672
Leu Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu
            210                 215                 220
```

```
gtg aag atc gct cct gac ctc acc agc cag gat aag gag gac att gcc      720
Val Lys Ile Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala
225             230              235              240

agt gtg gtc aaa gag ttg ggc atc gat ggg ctg att gtt acg aac acc      768
Ser Val Val Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr
                245              250              255

acc gtg agt cgc cct gcg ggc ctc cag ggt gcc ctg cgc tct gaa aca      816
Thr Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr
            260              265              270

gga ggg ctg agt ggg aag ccc ctc cgg gat tta tca act caa acc att      864
Gly Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile
            275              280              285

cgg gag atg tat gca ctc acc caa ggc cga gtt ccc ata att ggg gtt      912
Arg Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val
            290              295              300

ggt ggt gtg agc agc ggg cag gac gcg ctg gag aag atc cgg gca ggg      960
Gly Gly Val Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly
305             310              315              320

gcc tcc ctg gtg cag ctg tac acg gcc ctc acc ttc tgg ggg cca ccc     1008
Ala Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro
            325              330              335

gtt gtg ggc aaa gtc aag cgg gaa ctg gag gcc ctt ctg aaa gag cag     1056
Val Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln
            340              345              350

ggc ttt ggc gga gtc aca gat gcc att gga gca gat cat cgg agg         1101
Gly Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
            355              360              365
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<210> 22
<211> 367
<212> PRT
<213> Homo sapien

<400> 22
Met Ala Thr Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr
1               5                   10                  15
Leu Gln Gly Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg
            20                  25                  30
Phe Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp
            35                  40                  45
Met Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly
    50                  55                  60
Ile Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr
65                  70                  75                  80
Lys Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro
                85                  90                  95
Gln Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln
            100                 105                 110
Ala Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val
            115                 120                 125
Glu His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu
            130                 135                 140
```

```
Asp Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val
145                 150                 155                 160
Asp Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu
                165                 170                 175
Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu
                180                 185                 190
Arg Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val
            195                 200                 205
Leu Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu
    210                 215                 220
Val Lys Ile Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala
225                 230                 235                 240
Ser Val Val Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr
                245                 250                 255
Thr Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr
                260                 265                 270
Gly Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile
            275                 280                 285
Arg Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val
    290                 295                 300
Gly Gly Val Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly
305                 310                 315                 320
Ala Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro
                325                 330                 335
Val Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln
            340                 345                 350
Gly Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
            355                 360                 365
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<210> 23
<211> 1101
<212> DNA
<213> Homo sapien

<220>
<221> mutation
<222> 79
<223> C to G mutation

<221> mutation
<222> 80
<223> A to C mutation

<221> CDS
<222> (4)...(1101)
<223> His26Ala DHODH mutant

<300>
<301> Davis et al.
<302> Histidine to Alanine mutants of Human Dihydroorota
<303> Biochem. Pharmacol. (1997)
<304> 54
<306> 459-465

<400> 23
atg gcc acg gga gat gag cgt ttc tat gct gaa cac ctg atg ccg act      48
    Ala Thr Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr
    1               5                   10                  15


ctg cag ggg ctg ctg gac ccg gag tca gcc gcc aga ctg gct gtt cgc      96
Leu Gln Gly Leu Leu Asp Pro Glu Ser Ala Ala Arg Leu Ala Val Arg
                20                  25                  30
```

```
ttc acc tcc ctg ggg ctc ctt cca cgg gcc aga ttt caa gac tct gac     144
Phe Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp
            35                  40                  45

atg ctg gaa gtg aga gtt ctg ggc cat aaa ttc cga aat cca gta gga     192
Met Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly
            50                  55                  60

att gct gca gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat     240
Ile Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr
        65                  70                  75

aag atg ggc ttt ggt ttt gtt gag ata gga agt gtg act cca aaa cct     288
Lys Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro
    80                  85                  90                  95

cag gaa gga aac cct aga ccc aga gtc ttc cgc ctc cct gag gac caa     336
Gln Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln
                100                 105                 110

gct gtc att aac agg tat gga ttt aac agt cac ggg ctt tca gtg gtg     384
Ala Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val
                115                 120                 125

gaa cac agg tta cgg gcc aga cag cag aag cag gcc aag ctc aca gaa     432
Glu His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu
            130                 135                 140

gat gga ctg cct ctg ggg gtc aac ttg ggg aag aac aag acc tca gtg     480
Asp Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val
    145                 150                 155

gac gcc gcg gag gac tac gca gaa ggg gtg cgc gta ctg ggc ccc ctg     528
Asp Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu
160                 165                 170                 175

gcc gac tac ctg gtg gtg aat gtg tcc agc ccc aac act gcc ggg ctg     576
Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu
                180                 185                 190

cgg agc ctt cag gga aag gcc gag ctg cgc cgc ctg ctg acc aag gtg     624
Arg Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val
            195                 200                 205

ctg cag gag agg gat ggc ttg cgg aga gtg cac agg ccg gca gtc ctg     672
Leu Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu
            210                 215                 220

gtg aag atc gct cct gac ctc acc agc cag gat aag gag gac att gcc     720
Val Lys Ile Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala
    225                 230                 235

agt gtg gtc aaa gag ttg ggc atc gat ggg ctg att gtt acg aac acc     768
Ser Val Val Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr
240                 245                 250                 255

acc gtg agt cgc cct gcg ggc ctc cag ggt gcc ctg cgc tct gaa aca     816
Thr Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr
                260                 265                 270

gga ggg ctg agt ggg aag ccc ctc cgg gat tta tca act caa acc att     864
```

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Gly Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile
        275              280              285

cgg gag atg tat gca ctc acc caa ggc cga gtt ccc ata att ggg gtt    912
Arg Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val
        290              295              300

ggt ggt gtg agc agc ggg cag gac gcg ctg gag aag atc cgg gca ggg    960
Gly Gly Val Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly
        305              310              315

gcc tcc ctg gtg cag ctg tac acg gcc ctc acc ttc tgg ggg cca ccc    1008
Ala Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro
320              325              330              335

gtt gtg ggc aaa gtc aag cgg gaa ctg gag gcc ctt ctg aaa gag cag    1056
Val Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln
             340              345              350

ggc ttt ggc gga gtc aca gat gcc att gga gca gat cat cgg agg         1101
Gly Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
        355              360              365
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<210> 24
<211> 366
<212> PRT
<213> Homo sapien

<400> 24
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Ala Thr Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr Leu
1               5              10              15
Gln Gly Leu Leu Asp Pro Glu Ser Ala Ala Arg Leu Ala Val Arg Phe
        20              25              30
Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met
        35              40              45
Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile
        50              55              60
Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr Lys
65              70              75              80
Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro Gln
                85              90              95
Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln Ala
            100             105             110
Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val Glu
        115             120             125
His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu Asp
    130             135             140
Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val Asp
145             150             155             160
Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu Ala
            165             170             175
Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu Arg
        180             185             190
Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val Leu
        195             200             205
Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu Val
    210             215             220
Lys Ile Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala Ser
225             230             235             240
Val Val Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr Thr
            245             250             255
```

Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr Gly
           260   265   270

Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile Arg
           275   280   285

Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val Gly
    290   295   300

Gly Val Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly Ala
305   310   315   320

Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro Val
           325   330   335

Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln Gly
           340   345   350

Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
           355   360   365

<210> 25
<211> 1560
<212> DNA
<213> Aspergillus nidulans

<220>
<221> CDS
<222> (1)...(1560)
<223> Aspergillus nidulans Val200Glu mutant DHODH cDNA

<221> mutation
<222> 599
<223> T to A mutatation

<400> 25
atg gct acg aat tct ttc cga aaa ctc act ttt tca gga gcc tcc cgt   48
Met Ala Thr Asn Ser Phe Arg Lys Leu Thr Phe Ser Gly Ala Ser Arg
1   5   10   15

ctg ggt ggt tgt cgc cgt ctc cca cta acc tgc aga caa ctt cga ttc   96
Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe
            20   25   30

gcc tcc gac agc gga gcc gca gcg gca act aca aaa gca acg gcc gaa   144
Ala Ser Asp Ser Gly Ala Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu
        35   40   45

tca gca gcc gag tca gct agt ata aac gtc aaa gag gca ccc aaa aag   192
Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys
    50   55   60

gcc gga cgg ggc ctg cgg cgc acg gtc ctg gga acg tcg ttg gcg ctg   240
Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu
65   70   75   80

acg ctg ctg gtt gga tat gtc tac ggg acg gac acc cgg gcg agt gtg   288
Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val
                85   90   95

cat cgg tac ggt gtt gtg ccg ctg att aga gca ttg tat cct gat gcg   336
His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala
                100   105   110

gaa gat gcg cat cat att ggt gtc gat act tta aag atg ctg tat aag   384
Glu Asp Ala His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys
            115   120   125

```
tat ggt ctg cat cca agg gaa cgg ggg gat ccg gat gga gat ggg gcg    432
Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala
    130                 135             140

ctg gcg aca gag gtc ttt ggg tat aca ctg tca aac cca att ggc ata    480
Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile
145                 150             155                     160

tcg ggc ggc ctg gac aag cat gct gag atc cct gat ccg ctg ttc gcg    528
Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala
                165             170             175

atc ggt cct gcc att gtc gaa gtc ggg ggt acg aca ccc tta cca cag    576
Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln
            180             185             190

gat ggt aac ccg cgt cct cgc gaa ttc cga ctt cca tca cag aga gcg    624
Asp Gly Asn Pro Arg Pro Arg Glu Phe Arg Leu Pro Ser Gln Arg Ala
        195             200             205

atg ata aac cgg tac ggc ctc aac tcc aaa ggc gca gat cac atg gca    672
Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala
        210             215             220

gct atc ttg gag caa cga gta cgc gat ttt gcc tac gca aac gga ttt    720
Ala Ile Leu Glu Gln Arg Val Arg Asp Phe Ala Tyr Ala Asn Gly Phe
225             230             235             240

ggg gca tac gat gcg gct aag cag cgt gta ttg gac ggc gaa gct ggt    768
Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly
            245             250             255

gtg cca cca ggt agt ctt cag cct ggt aag ctt tta gct gtc caa gtg    816
Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val
            260             265             270

gca aag aac aag gcc act cct gac ggc gac att gaa gcc atc aag cgc    864
Ala Lys Asn Lys Ala Thr Pro Asp Gly Asp Ile Glu Ala Ile Lys Arg
        275             280             285

gac tat gtg tat tgc gtg gac cgt gtg gcc aaa tac gct gat att ctt    912
Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu
        290             295             300

gtt gtg aat gta tcg agc ccc aac aca ccc ggt ctc cgt gac ctt caa    960
Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln
305             310             315             320

gcc act gcc ccg ctc aca gct atc ttg agt gct gtc gtt ggc gcg gca    1008
Ala Thr Ala Pro Leu Thr Ala Ile Leu Ser Ala Val Val Gly Ala Ala
            325             330             335

aag agc gtg aac cgc aag acc aaa cca tat gtt atg gtc aag gtc agt    1056
Lys Ser Val Asn Arg Lys Thr Lys Pro Tyr Val Met Val Lys Val Ser
        340             345             350

ccg gat gaa gac tca gat gaa caa gtc tct ggt atc tgc gac gcc gtc    1104
Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val
        355             360             365

cga gca tcc ggt gtc gac gga gtg att gtc gga aac aca aca aac cgt    1152
Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg
```

```
          370                    375                    380
cgc ccc gac cct ata ccc caa ggt tac act ctt ccg gcc aag gag cag    1200
Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln
385                 390                 395                 400

gca acg ttg aaa gaa acc ggc ggg tat tca ggt cca cag ctg ttc gat    1248
Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp
                405                 410                 415

cgc aca gtg gcc ctt gtg gct cgg tac cgc tcc atg ctg gat gcg gag    1296
Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu
            420                 425                 430

tcg gaa acg gcc gga tcc gcc aag gat tca gca gcg acc ata gcg caa    1344
Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln
            435                 440                 445

aca gag cca ggc tcg gaa aac gtt cct cct gtg gaa gcg cca agc gga    1392
Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly
        450                 455                 460

ctg ccg cgc aaa gtt atc ttc gct tcg ggt ggt atc acc aac ggg aag    1440
Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys
465                 470                 475                 480

cag gct cac gct gtt tta gac aca ggg gca tct gtt gcc atg atg tac    1488
Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr
                485                 490                 495

acc ggt gtg gtc tat ggt ggc gtc ggc act gtc act cga gtg aag caa    1536
Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln
            500                 505                 510

gaa ctt cga acg gcg aaa aag gag                                     1560
Glu Leu Arg Thr Ala Lys Lys Glu
        515                 520
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<210> 26
<211> 520
<212> PRT
<213> Aspergillus nidulans

<400> 26
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Met Ala Thr Asn Ser Phe Arg Lys Leu Thr Phe Ser Gly Ala Ser Arg
1               5                   10                  15
Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe
            20                  25                  30
Ala Ser Asp Ser Gly Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu
        35                  40                  45
Ser Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys
    50                  55                  60
Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu
65                  70                  75                  80
Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val
                85                  90                  95
His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala
            100                 105                 110
Glu Asp Ala His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys
        115                 120                 125
Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala
```

```
            130                      135                      140
Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile
145                      150                      155                      160
Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala
                 165                      170                      175
Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln
                 180                      185                      190
Asp Gly Asn Pro Arg Pro Arg Glu Phe Arg Leu Pro Ser Gln Arg Ala
                 195                      200                      205
Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala
210                      215                      220
Ala Ile Leu Glu Gln Arg Val Arg Asp Phe Ala Tyr Ala Asn Gly Phe
225                      230                      235                      240
Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly
                 245                      250                      255
Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val
                 260                      265                      270
Ala Lys Asn Lys Ala Thr Pro Asp Gly Asp Ile Glu Ala Ile Lys Arg
                 275                      280                      285
Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu
                 290                      295                      300
Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln
305                      310                      315                      320
Ala Thr Ala Pro Leu Thr Ala Ile Leu Ser Ala Val Val Gly Ala Ala
                 325                      330                      335
Lys Ser Val Asn Arg Lys Thr Lys Pro Tyr Val Met Val Lys Val Ser
                 340                      345                      350
Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val
                 355                      360                      365
Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg
370                      375                      380
Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln
385                      390                      395                      400
Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp
                 405                      410                      415
Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu
                 420                      425                      430
Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln
                 435                      440                      445
Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly
450                      455                      460
Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys
465                      470                      475                      480
Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr
                 485                      490                      495
Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln
                 500                      505                      510
Glu Leu Arg Thr Ala Lys Lys Glu
                 515                      520
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<210> 27
<211> 1560
<212> DNA
<213> Aspergillus nidulans

<220>
<221> CDS
<222> (1)...(1560)
<223> Aspergillus nidulans Ala115Val mutant DHODH cDNA

<221> mutation
<222> 344

<223> C to T mutation

<400> 27

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atg gct acg aat tct ttc cga aaa ctc act ttt tca gga gcc tcc cgt        48
Met Ala Thr Asn Ser Phe Arg Lys Leu Thr Phe Ser Gly Ala Ser Arg
 1               5                  10                  15

ctg ggt ggt tgt cgc cgt ctc cca cta acc tgc aga caa ctt cga ttc        96
Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe
                20                  25                  30

gcc tcc gac agc gga gcc gca gcg gca act aca aaa gca acg gcc gaa       144
Ala Ser Asp Ser Gly Ala Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu
             35                  40                  45

tca gca gcc gag tca gct agt ata aac gtc aaa gag gca ccc aaa aag       192
Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys
         50                  55                  60

gcc gga cgg ggc ctg cgg cgc acg gtc ctg gga acg tcg ttg gcg ctg       240
Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu
 65                  70                  75                  80

acg ctg ctg gtt gga tat gtc tac ggg acg gac acc cgg gcg agt gtg       288
Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val
                 85                  90                  95

cat cgg tac ggt gtt gtg ccg ctg att aga gca ttg tat cct gat gcg       336
His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala
                100                 105                 110

gaa gat gtg cat cat att ggt gtc gat act tta aag atg ctg tat aag       384
Glu Asp Val His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys
            115                 120                 125

tat ggt ctg cat cca agg gaa cgg ggg gat ccg gat gga gat ggg gcg       432
Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala
        130                 135                 140

ctg gcg aca gag gtc ttt ggg tat aca ctg tca aac cca att ggc ata       480
Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile
145                 150                 155                 160

tcg ggc ggc ctg gac aag cat gct gag atc cct gat ccg ctg ttc gcg       528
Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala
                165                 170                 175

atc ggt cct gcc att gtc gaa gtc ggg ggt acg aca ccc tta cca cag       576
Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln
                180                 185                 190

gat ggt aac ccg cgt cct cgc gta ttc cga ctt cca tca cag aga gcg       624
Asp Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Ser Gln Arg Ala
            195                 200                 205

atg ata aac cgg tac ggc ctc aac tcc aaa ggc gca gat cac atg gca       672
Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala
        210                 215                 220

gct atc ttg gag caa cga gta cgc gat ttt gcc tac gca aac gga ttt       720
Ala Ile Leu Glu Gln Arg Val Arg Asp Phe Ala Tyr Ala Asn Gly Phe
225                 230                 235                 240
```

```
ggg gca tac gat gcg gct aag cag cgt gta ttg gac ggc gaa gct ggt       768
Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly
            245             250             255

gtg cca cca ggt agt ctt cag cct ggt aag ctt tta gct gtc caa gtg       816
Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val
            260             265             270

gca aag aac aag gcc act cct gac ggc gac att gaa gcc atc aag cgc       864
Ala Lys Asn Lys Ala Thr Pro Asp Gly Asp Ile Glu Ala Ile Lys Arg
            275             280             285

gac tat gtg tat tgc gtg gac cgt gtg gcc aaa tac gct gat att ctt       912
Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu
            290             295             300

gtt gtg aat gta tcg agc ccc aac aca ccc ggt ctc cgt gac ctt caa       960
Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln
305             310             315             320

gcc act gcc ccg ctc aca gct atc ttg agt gct gtc gtt ggc gcg gca      1008
Ala Thr Ala Pro Leu Thr Ala Ile Leu Ser Ala Val Val Gly Ala Ala
            325             330             335

aag agc gtg aac cgc aag acc aaa cca tat gtt atg gtc aag gtc agt      1056
Lys Ser Val Asn Arg Lys Thr Lys Pro Tyr Val Met Val Lys Val Ser
            340             345             350

ccg gat gaa gac tca gat gaa caa gtc tct ggt atc tgc gac gcc gtc      1104
Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val
            355             360             365

cga gca tcc ggt gtc gac gga gtg att gtc gga aac aca aca aac cgt      1152
Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg
            370             375             380

cgc ccc gac cct ata ccc caa ggt tac act ctt ccg gcc aag gag cag      1200
Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln
385             390             395             400

gca acg ttg aaa gaa acc ggc ggg tat tca ggt cca cag ctg ttc gat      1248
Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp
            405             410             415

cgc aca gtg gcc ctt gtg gct cgg tac cgc tcc atg ctg gat gcg gag      1296
Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu
            420             425             430

tcg gaa acg gcc gga tcc gcc aag gat tca gca gcg acc ata gcg caa      1344
Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln
            435             440             445

aca gag cca ggc tcg gaa aac gtt cct cct gtg gaa gcg cca agc gga      1392
Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly
            450             455             460

ctg ccg cgc aaa gtt atc ttc gct tcg ggt ggt atc acc aac ggg aag      1440
Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys
465             470             475             480

cag gct cac gct gtt tta gac aca ggg gca tct gtt gcc atg atg tac      1488
```

```
Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr
                485                 490                 495

acc ggt gtg gtc tat ggt ggc gtc ggc act gtc act cga gtg aag caa      1536
Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln
                500                 505                 510

gaa ctt cga acg gcg aaa aag gag                                      1560
Glu Leu Arg Thr Ala Lys Lys Glu
                515                 520
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<210> 28
<211> 520
<212> PRT
<213> Aspergillus nidulans

<400> 28
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Met Ala Thr Asn Ser Phe Arg Lys Leu Thr Phe Ser Gly Ala Ser Arg
  1               5                  10                  15
Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe
             20                  25                  30
Ala Ser Asp Ser Gly Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu
             35                  40                  45
Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys
         50                  55                  60
Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu
 65                  70                  75                  80
Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val
                 85                  90                  95
His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala
             100                 105                 110
Glu Asp Val His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys
         115                 120                 125
Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala
         130                 135                 140
Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile
 145                 150                 155                 160
Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala
                 165                 170                 175
Ile Gly Pro Ala Ile Val Glu Val Gly Thr Thr Pro Leu Pro Gln
             180                 185                 190
Asp Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Ser Gln Arg Ala
         195                 200                 205
Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala
         210                 215                 220
Ala Ile Leu Glu Gln Arg Val Arg Asp Phe Ala Tyr Ala Asn Gly Phe
 225                 230                 235                 240
Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly
             245                 250                 255
Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val
             260                 265                 270
Ala Lys Asn Lys Ala Thr Pro Asp Gly Asp Ile Glu Ala Ile Lys Arg
         275                 280                 285
Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu
         290                 295                 300
Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln
 305                 310                 315                 320
Ala Thr Ala Pro Leu Thr Ala Ile Leu Ser Ala Val Val Gly Ala Ala
             325                 330                 335
Lys Ser Val Asn Arg Lys Thr Lys Pro Tyr Val Met Val Lys Val Ser
         340                 345                 350
```

```
Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val
    355                     360                 365
Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg
    370                 375                 380
Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln
385                 390                 395                 400
Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp
                405                 410                 415
Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu
                420                 425                 430
Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln
                435                 440                 445
Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly
    450                 455                 460
Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys
465                 470                 475                 480
Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr
                485                 490                 495
Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln
            500                 505                 510
Glu Leu Arg Thr Ala Lys Lys Glu
    515                 520
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<210> 29
<211> 1707
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (67)...(1611)
<223> wild-type IMP dehyrdogenase cDNA

<400> 29

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cctctgcggc gcggtcctcg gagcggcgcg gttctcggag ccacgcgtct gtcttcctcc    60
gtggtc atg gcg gac tac ctg att agc gga ggc acc tct tac gtg ccg      108
        Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro
        1               5                   10

gac gac ggg ctc aca gcg cag cag ctc ttc aac tgc ggg gac ggc ctc    156
Asp Asp Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu
15                  20                  25                  30

acc tac aat gat ttt ctc att ctt cct ggg tat atc gac ttc act gca    204
Thr Tyr Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala
                35                  40                  45

gat cag gtg gac ttg acg tct gct cta act aag aag att aca cta aag    252
Asp Gln Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys
                50                  55                  60

acc cca ttg gtt tcc tca ccc atg gac act gtc aca gag gct gga atg    300
Thr Pro Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met
            65                  70                  75

gcc atc gcg atg gcg ctt aca gga ggt att ggt ttc atc cac cac aac    348
Ala Ile Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn
        80                  85                  90

tgc aca cct gaa ttc cag gcc aat gaa gtt cgg aaa gtg aag aaa tac    396
Cys Thr Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr
95                  100                 105                 110
```

```
gaa cag gga ttc atc act gac ccc gtg gtc ctt agc ccc aag gat cgt      444
Glu Gln Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg
                115             120             125

gta cgc gat gtt ttt gag gcc aaa gcc agg cat ggc ttc tgt ggt atc      492
Val Arg Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile
                130             135             140

ccc atc aca gat aca ggc cgg atg ggg agt cga ttg gtg ggc atc atc      540
Pro Ile Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile
                145             150             155

tcc tca agg gac att gat ttc ctc aag gag gaa gag cat gac cgg ttc      588
Ser Ser Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Arg Phe
    160             165             170

ttg gaa gag atc atg act aag agg gaa gat ttg gtg gtc gcc cct gcc      636
Leu Glu Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Ala
175             180             185             190

ggc gtc act ctg aaa gag gca aat gag att ctg cag cga agt aaa aag      684
Gly Val Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys
                195             200             205

gga aag ttg ccc att gtg aat gaa aat gat gag ctg gta gcc atc att      732
Gly Lys Leu Pro Ile Val Asn Glu Asn Asp Glu Leu Val Ala Ile Ile
                210             215             220

gcc cgg aca gac cta aag aag aat cgt gat tac ccc ctg gcc tcc aaa      780
Ala Arg Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys
                225             230             235

gat gcc aag aag caa ctg ctg tgt ggg gca gcc att ggc act cat gag      828
Asp Ala Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu
    240             245             250

gat gac aag tat agg ctg gac tta ctg gcc ctt gct ggt gtg gat gta      876
Asp Asp Lys Tyr Arg Leu Asp Leu Leu Ala Leu Ala Gly Val Asp Val
255             260             265             270

gtg gtt ttg gac tct tcc cag gga aac tcc atc ttc caa atc aat atg      924
Val Val Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met
                275             280             285

atc aaa tac atc aag gag aag tat ccc agt cta cag gtc att gga ggc      972
Ile Lys Tyr Ile Lys Glu Lys Tyr Pro Ser Leu Gln Val Ile Gly Gly
                290             295             300

aat gta gtc act gct gcg caa gcc aag aac ctc ata gat gca ggt gta     1020
Asn Val Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val
                305             310             315

gat gct ttg cga gtc ggc atg gga agt ggt tcc atc tgc atc acc cag     1068
Asp Ala Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln
                320             325             330

gaa gtg ttg gcc tgt ggg cgg ccc caa gcc aca gca gtg tac aag gtc     1116
Glu Val Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val
335             340             345             350

tct gag tat gcc cgt cgc ttt ggt gtt cct gtt att gct gat gga gga     1164
```

```
Ser Glu Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly
            355                 360                 365

atc caa aat gtg ggt cat att gcc aaa gct ttg gct ctt ggg gct tcc    1212
Ile Gln Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser
            370                 375                 380

aca gtc atg atg ggc tcc ctc ctg gct gcc acc act gag gcc cct ggc    1260
Thr Val Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly
            385                 390                 395

gag tac ttc ttc tca gat ggg atc cgg ctg aag aaa tac cga ggt atg    1308
Glu Tyr Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met
        400                 405                 410

ggt tct ctt gat gcc atg gac aaa cat ctc agc agc cag aac cga tac    1356
Gly Ser Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr
415                 420                 425                 430

ttc agt gaa gct gac aaa atc aaa gtg gcc caa gga gtt tca ggg gca    1404
Phe Ser Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala
                435                 440                 445

gtg cag gac aag ggg tct atc cac aag ttc gtt cct tac ctg att gct    1452
Val Gln Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala
                450                 455                 460

ggc atc cag cat tcc tgt caa gac att ggt gcc aag agt tta acc caa    1500
Gly Ile Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln
                465                 470                 475

gtc aga gcc atg acg tac tcg ggg gag ctt aaa ttt gag aag agg aca    1548
Val Arg Ala Met Thr Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr
        480                 485                 490

tcc tct gct cag gtg gaa ggt ggc gtc cac agc ctc cat tcg tac gag    1596
Ser Ser Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu
495                 500                 505                 510

aaa cgg ctt ttc tga aaacagatcc agtatatgcc ttgaattttt caataaaagt    1651
Lys Arg Leu Phe  *


ttgggaaaaa aaagtgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa        1707
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<210> 30
<211> 514
<212> PRT
<213> Mus musculus

<400> 30
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Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
1               5                   10                  15
Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
            20                  25                  30
Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
            35                  40                  45
Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
        50                  55                  60
Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
65                  70                  75                  80
Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
```

```
                         85                        90                        95
Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
                100                       105                       110
Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
        115                       120                       125
Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
        130                       135                       140
Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
145                       150                       155                       160
Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Arg Phe Leu Glu
                165                       170                       175
Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Ala Gly Val
                180                       185                       190
Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
        195                       200                       205
Leu Pro Ile Val Asn Glu Asn Asp Glu Leu Val Ala Ile Ile Ala Arg
210                       215                       220
Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
225                       230                       235                       240
Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
                245                       250                       255
Lys Tyr Arg Leu Asp Leu Leu Ala Leu Ala Gly Val Asp Val Val Val
                260                       265                       270
Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
        275                       280                       285
Tyr Ile Lys Glu Lys Tyr Pro Ser Leu Gln Val Ile Gly Gly Asn Val
        290                       295                       300
Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
305                       310                       315                       320
Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val
                325                       330                       335
Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu
                340                       345                       350
Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
                355                       360                       365
Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
370                       375                       380
Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
385                       390                       395                       400
Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
                405                       410                       415
Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser
                420                       425                       430
Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
                435                       440                       445
Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
        450                       455                       460
Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg
465                       470                       475                       480
Ala Met Thr Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser
                485                       490                       495
Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg
                500                       505                       510
Leu Phe
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<210> 31
<211> 1707
<212> DNA
<213> Mus musculus

<220>

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<221> CDS
<222> (67)...(1611)
<223> mouse IMP dehydrogenase cDNA double mutant:
      Thr333Ile
      Ser351Tyr

<221> mutation
<222> 1064
<223> C to T mutation

<221> mutation
<222> 1118
<223> C to A mutation

<400> 31
cctctgcggc gcggtcctcg gagcggcgcg gttctcggag ccacgcgtct gtcttcctcc      60
gtggtc atg gcg gac tac ctg att agc gga ggc acc tct tac gtg ccg        108
       Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro
        1               5                   10

gac gac ggg ctc aca gcg cag cag ctc ttc aac tgc ggg gac ggc ctc      156
Asp Asp Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu
15                  20                  25                  30

acc tac aat gat ttt ctc att ctt cct ggg tat atc gac ttc act gca      204
Thr Tyr Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala
                35                  40                  45

gat cag gtg gac ttg acg tct gct cta act aag aag att aca cta aag      252
Asp Gln Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys
                50                  55                  60

acc cca ttg gtt tcc tca ccc atg gac act gtc aca gag gct gga atg      300
Thr Pro Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met
            65                  70                  75

gcc atc gcg atg gcg ctt aca gga ggt att ggt ttc atc cac cac aac      348
Ala Ile Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn
        80                  85                  90

tgc aca cct gaa ttc cag gcc aat gaa gtt cgg aaa gtg aag aaa tac      396
Cys Thr Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr
95                  100                 105                 110

gaa cag gga ttc atc act gac ccc gtg gtc ctt agc ccc aag gat cgt      444
Glu Gln Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg
                115                 120                 125

gta cgc gat gtt ttt gag gcc aaa gcc agg cat ggc ttc tgt ggt atc      492
Val Arg Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile
                130                 135                 140

ccc atc aca gat aca ggc cgg atg ggg agt cga ttg gtg ggc atc atc      540
Pro Ile Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile
                145                 150                 155

tcc tca agg gac att gat ttc ctc aag gag gaa gag cat gac cgg ttc      588
Ser Ser Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Arg Phe
160                 165                 170

ttg gaa gag atc atg act aag agg gaa gat ttg gtg gtc gcc cct gcc      636
Leu Glu Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Ala
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         175                      180                      185                      190
ggc gtc act ctg aaa gag gca aat gag att ctg cag cga agt aaa aag        684
Gly Val Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys
                195                      200                      205

gga aag ttg ccc att gtg aat gaa aat gat gag ctg gta gcc atc att        732
Gly Lys Leu Pro Ile Val Asn Glu Asn Asp Glu Leu Val Ala Ile Ile
                    210                      215                      220

gcc cgg aca gac cta aag aag aat cgt gat tac ccc ctg gcc tcc aaa        780
Ala Arg Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys
                225                      230                      235

gat gcc aag aag caa ctg ctg tgt ggg gca gcc att ggc act cat gag        828
Asp Ala Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu
        240                      245                      250

gat gac aag tat agg ctg gac tta ctg gcc ctt gct ggt gtg gat gta        876
Asp Asp Lys Tyr Arg Leu Asp Leu Leu Ala Leu Ala Gly Val Asp Val
255                      260                      265                      270

gtg gtt ttg gac tct tcc cag gga aac tcc atc ttc caa atc aat atg        924
Val Val Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met
                    275                      280                      285

atc aaa tac atc aag gag aag tat ccc agt cta cag gtc att gga ggc        972
Ile Lys Tyr Ile Lys Glu Lys Tyr Pro Ser Leu Gln Val Ile Gly Gly
                290                      295                      300

aat gta gtc act gct gcg caa gcc aag aac ctc ata gat gca ggt gta       1020
Asn Val Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val
        305                      310                      315

gat gct ttg cga gtc ggc atg gga agt ggt tcc atc tgc atc atc cag       1068
Asp Ala Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Ile Gln
        320                      325                      330

gaa gtg ttg gcc tgt ggg cgg ccc caa gcc aca gca gtg tac aag gtc       1116
Glu Val Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val
335                      340                      345                      350

tat gag tat gcc cgt cgc ttt ggt gtt cct gtt att gct gat gga gga       1164
Tyr Glu Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly
                    355                      360                      365

atc caa aat gtg ggt cat att gcc aaa gct ttg gct ctt ggg gct tcc       1212
Ile Gln Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser
                370                      375                      380

aca gtc atg atg ggc tcc ctc ctg gct gcc acc act gag gcc cct ggc       1260
Thr Val Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly
                385                      390                      395

gag tac ttc ttc tca gat ggg atc cgg ctg aag aaa tac cga ggt atg       1308
Glu Tyr Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met
        400                      405                      410

ggt tct ctt gat gcc atg gac aaa cat ctc agc agc cag aac cga tac       1356
Gly Ser Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr
415                      420                      425                      430
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ttc agt gaa gct gac aaa atc aaa gtg gcc caa gga gtt tca ggg gca      1404
Phe Ser Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala
            435             440             445

gtg cag gac aag ggg tct atc cac aag ttc gtt cct tac ctg att gct      1452
Val Gln Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala
            450             455             460

ggc atc cag cat tcc tgt caa gac att ggt gcc aag agt tta acc caa      1500
Gly Ile Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln
            465             470             475

gtc aga gcc atg acg tac tcg ggg gag ctt aaa ttt gag aag agg aca      1548
Val Arg Ala Met Thr Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr
        480             485             490

tcc tct gct cag gtg gaa ggt ggc gtc cac agc ctc cat tcg tac gag      1596
Ser Ser Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu
495             500             505             510

aaa cgg ctt ttc tga aaacagatcc agtatatgcc ttgaattttt caataaaagt     1651
Lys Arg Leu Phe  *


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<212> PRT
<213> Mus musculus

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            20                  25                  30
Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
            35                  40                  45
Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
        50                  55                  60
Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
65                  70                  75                  80
Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
                85                  90                  95
Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
            100                 105                 110
Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
        115                 120                 125
Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
        130                 135                 140
Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
145                 150                 155                 160
Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Arg Phe Leu Glu
                165                 170                 175
Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Ala Gly Val
            180                 185                 190
Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
        195                 200                 205
Leu Pro Ile Val Asn Glu Asn Asp Glu Leu Val Ala Ile Ile Ala Arg
    210                 215                 220
Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
225                 230                 235                 240
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Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
            245                     250                     255
Lys Tyr Arg Leu Asp Leu Leu Ala Leu Ala Gly Val Asp Val Val Val
            260                     265                     270
Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
            275                     280                     285
Tyr Ile Lys Glu Lys Tyr Pro Ser Leu Gln Val Ile Gly Gly Asn Val
    290                     295                     300
Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
305                     310                     315                 320
Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Ile Gln Glu Val
            325                     330                     335
Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Tyr Glu
            340                     345                     350
Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
            355                     360                     365
Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
    370                     375                     380
Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
385                     390                     395                 400
Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
            405                     410                     415
Leu Asp Ala Met Asp Lys His Leu Ser Gln Asn Arg Tyr Phe Ser
            420                     425                     430
Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
            435                     440                     445
Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
    450                     455                     460
Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg
465                     470                     475                 480
Ala Met Thr Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser
            485                     490                     495
Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg
            500                     505                     510
Leu Phe
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<210> 33
<211> 5627
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Sequence of pMG
      plasmid from InvivoGen

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tttgtgatgc tattgcttta tttgtgaaat ttgtgatgct attgctttat ttgtaaccat 180
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<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Forward primer for amplification-
based cloning of hIMPDH type II cDNA

<400> 34
gctatctgca ggccgccacc atggccgact acctgattag   40

<210> 35
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Reverse primer for amplification-
based cloning of hIMPDH type II cDNA

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catactcttc gccgaaaaga ctagatctcg atc   33

<210> 36
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Forward primer for T333I mutation
of hIMPDH type II cDNA

<400> 36
ggctccatct gcattatcca ggaagtgctg gc   32

<210> 37
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Reverse primer for T333I mutation
of hIMPDH type II cDNA

<400> 37
ccgaggtaga cgtaataggt ccttcacgac cg   32

<210> 38
<211> 38
<212> DNA
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<220>
<223> Description of Artificial Sequence: Forward primer for S351Y mutation
of hIMPDH type II cDNA

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<223> Description of Artificial Sequence: Reverse primer for S351Y mutation
of hIMPDH type II cDNA

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